

Thu Jun 24 08:47:52 2004

epper526106.pep.ram

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:08:03 ; Search time 184 Seconds  
(without alignments)  
1395.120 Million cell updates/sec

Title: EPPER526106.PEP  
Perfect score: 1345  
Sequence: 1 hpetlvkvkaedqlgarvg.....tmdermrqiaiegslkhw 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 6019581 seqs, 976053577 residues  
Total number of hits satisfying chosen parameters: 6019581

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents AA Main:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1330	98.9	263	22	US-09-764-163A-2	Sequence 2, Appli
3	1330	98.9	263	22	US-09-791-537-90233	Sequence 90233, A
4	1330	98.9	263	31	US-10-668-778-2	Sequence 2, Appli
5	1330	98.9	286	1	PCT-US02-12405-523	Sequence 523, App
6	1330	98.9	286	1	PCT-US99-17440-7	Sequence 7, Appli
7	1330	98.9	286	1	PCT-US99-17440-14	Sequence 14, Appl
8	1330	98.9	286	15	US-09-129-611-7	Sequence 21, Appl
9	1330	98.9	286	15	US-09-129-611-14	Sequence 7, Appli
10	1330	98.9	286	15	US-09-129-611-21	Sequence 14, Appl
11	1330	98.9	286	15	US-09-129-611-21	Sequence 21, Appl
12	1330	98.9	286	18	US-09-490-070-265	Sequence 265, App
13	1330	98.9	286	18	US-09-490-070-362	Sequence 362, App
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19	1330	98.9	286	23	US-09-837-306-354	Sequence 354, App
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21	1330	98.9	286	25	US-09-980-585A-4	Sequence 4, Appli
22	1330	98.9	286	26	US-10-045-674-523	Sequence 523, App
23	1330	98.9	286	27	US-10-191-966-7	Sequence 7, Appli
24	1330	98.9	286	27	US-10-191-966-14	Sequence 14, Appl
25	1330	98.9	286	27	US-10-191-966-21	Sequence 21, Appl
26	1330	98.9	286	30	US-10-405-027-3366	Sequence 3366, App
27	1330	98.9	286	30	US-10-405-027-3369	Sequence 3369, App
28	1330	98.9	286	30	US-10-405-027-4786	Sequence 4786, App
29	1330	98.9	290	1	PCT-US01-01239-1215	Sequence 1215, App
30	1330	98.9	290	1	PCT-US01-01354-11955	Sequence 11955, A
31	1330	98.9	290	22	US-09-764-902-1215	Sequence 1215, App
32	1330	98.9	290	22	US-09-764-905-11955	Sequence 11955, A
33	1330	98.9	290	26	US-10-092-399-11955	Sequence 11955, A
34	1330	98.9	299	18	US-09-490-070-285	Sequence 285, App
35	1330	98.9	299	18	US-09-490-070-298	Sequence 298, App
36	1330	98.9	299	18	US-09-490-070-300	Sequence 300, App
37	1330	98.9	299	18	US-09-490-070A-285	Sequence 285, App
38	1330	98.9	299	18	US-09-490-070A-298	Sequence 298, App
39	1330	98.9	299	18	US-09-490-070A-300	Sequence 300, App
40	1330	98.9	299	18	US-09-490-153-285	Sequence 285, App
41	1330	98.9	299	18	US-09-490-153-298	Sequence 298, App
42	1330	98.9	299	18	US-09-490-153-300	Sequence 300, App
43	1330	98.9	2307	1	PCT-US99-17440-2	Sequence 2, Appli
44	1330	98.9	2307	1	PCT-US99-17440-9	Sequence 9, Appli
45	1330	98.9	2307	1	PCT-US99-17440-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1  
US-09-526-106-2  
; Sequence 2, Application US/09526106  
; GENERAL INFORMATION:  
; APPLICANT: Balint, Robert F.  
; APPLICANT: Her, Jeng-Hong  
; APPLICANT: Kalobios, Inc.  
; TITLE OF INVENTION: Interaction-Activated Proteins  
; FILE REFERENCE: 021167-000700US  
; CURRENT APPLICATION NUMBER: US/09/526,106  
; CURRENT FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: US 60/124,339  
; PRIOR FILING DATE: 1999-03-15  
; PRIOR APPLICATION NUMBER: US 60/135,926  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: US 60/175,968  
; PRIOR FILING DATE: 2000-01-13  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: Escherichia coli

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; FEATURE:
; OTHER INFORMATION: TEM-1 beta-lactamase
US-09-526-106-2

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; RESULT 2
US-09-764-163A-2
; Sequence 2, Application US/09764163A
; GENERAL INFORMATION:
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Horng
; APPLICANT: Kalobios, Inc.
; TITLE OF INVENTION: Circularly Permuted, Interaction-Activated Proteins
; FILE REFERENCE: 021167-000710US
; CURRENT APPLICATION NUMBER: US/09/764,163A
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/175,968
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: US 09/526,106
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Escherichia coli
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; OTHER INFORMATION: TEM-1 beta-lactamase
US-09-764-163A-2

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Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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; RESULT 3
US-09-791-537-90233
; Sequence 90233, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMEBI
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90233
; LENGTH: 263
; TYPE: PRT
; ORGANISM: pdb 1BTL
US-09-791-537-90233

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US-10-668-778-2
; Sequence 2, Application US/10668778
; GENERAL INFORMATION:
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Horng
; APPLICANT: Kalobios, Inc.
; TITLE OF INVENTION: Interaction-Activated Proteins
; FILE REFERENCE: 021167-000700US
; CURRENT APPLICATION NUMBER: US/10/668,778
; CURRENT FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: US/09/526,106
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/124,339
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: US 60/135,926
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 60/175,968
; PRIOR FILING DATE: 2000-01-13
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
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LENGTH: 263  
TYPE: PRT  
ORGANISM: Escherichia coli  
FEATURE:  
OTHER INFORMATION: TEM-1 beta-lactamase  
US-10-668-778-2

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Best Local Similarity 98.9%; Pred. No. 5.2e-132;  
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RESULT 5

PCT-US02-12405-523  
Sequence 523, Application PC/TUS0212405  
GENERAL INFORMATION:  
APPLICANT: LADNER, ROBERT C.  
APPLICANT: COHEN, EDWARD H.  
APPLICANT: NASTRI, HORACIO G.  
APPLICANT: ROOKEY, KRISTIN L.  
APPLICANT: HOET, RENE  
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.  
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING  
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY  
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL  
TITLE OF INVENTION: LIBRARIES  
FILE REFERENCE: DYAX/002 CIP2  
CURRENT APPLICATION NUMBER: PCT/US02/12405  
CURRENT FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: 06/198,069  
PRIOR FILING DATE: 2000-04-17  
PRIOR APPLICATION NUMBER: 09/837,306  
PRIOR FILING DATE: 2001-04-17  
NUMBER OF SEQ ID NOS: 635  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 523  
LENGTH: 286  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS  
OTHER INFORMATION: protein sequence  
PCT-US02-12405-523

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Best Local Similarity 98.9%; Pred. No. 6e-132;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 204 QLIDWMEADKVAAGPLLRSAIPAGWFIADKSGAGERSRGIITIALGPDGKPSRIVITYTTG 263  
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Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 6  
PCT-US99-17440-7

Sequence 7, Application PC/TUS9917440  
GENERAL INFORMATION:  
APPLICANT: Potts, Karen E.  
APPLICANT: Jackson, Roberta L.  
APPLICANT: Patrick, Amy K.  
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
FILE REFERENCE: 0125-0005A  
CURRENT APPLICATION NUMBER: PCT/US99/17440  
CURRENT FILING DATE: 1999-08-02  
EARLIER APPLICATION NUMBER: 09/129,611  
EARLIER FILING DATE: 1998-08-05  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 7  
LENGTH: 286  
TYPE: PRT  
ORGANISM: Artificial Sequence  
PCT-US99-17440-7

Query Match 98.9%; Score 1330; DB 1; Length 286;  
Best Local Similarity 98.9%; Pred. No. 6e-132;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGILESFRSEERFPMMSTFKVLLCGAVLSRID 83  
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Db 84 AGQEQIGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
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QY 241 SQATMDERNRQIAEIGASLIKHW 263  
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RESULT 7  
PCT-US99-17440-14

Sequence 14, Application PC/TUS9917440  
GENERAL INFORMATION:  
APPLICANT: Potts, Karen E.  
APPLICANT: Jackson, Roberta L.  
APPLICANT: Patrick, Amy K.  
TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
FILE REFERENCE: 0125-0005A

; CURRENT APPLICATION NUMBER: PCT/US99/17440
; CURRENT FILING DATE: 1999-08-02
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
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Db 84 AGQEQLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143
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Db 144 KETLAFILNMGDHVTIRLDREWEPELNEAIPNDERDITTPVAMATTIRKLITGELLTLASRQ 203
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Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITIALGPDGKPSRIWIYTTG 263
QY 241 SQATMDERNRQIAEIGASLIKHW 263
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 8
PCT-US99-17440-21
; Sequence 21, Application PC/TUS9917440
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: PCT/US99/17440
; CURRENT FILING DATE: 1999-08-02
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
PCT-US99-17440-21

Query Match 98.9%; Score 1330; DB 1; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSFRRSEERFPMSTFKVLLCGAVLSRID 60
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
Db 84 AGQEQLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143
QY 121 KETLAFILNMGDHVTIRLDREWEPELNEAIPNDERDITTPVAMATTIRKLITGELLTLASRQ 180

Db 144 KETLAFILNMGDHVTIRLDREWEPELNEAIPNDERDITTPVAMATTIRKLITGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITIALGPDGKPSRIWIYTTG 240
Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITIALGPDGKPSRIWIYTTG 263
QY 241 SQATMDERNRQIAEIGASLIKHW 263
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 9
US-09-129-611-7
; Sequence 7, Application US/09129611A
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/129,611A
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-129-611-7

Query Match 98.9%; Score 1330; DB 15; Length 286;
Best Local Similarity 98.9%; Pred. No. 6e-132;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSFRRSEERFPMSTFKVLLCGAVLSRID 60
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
Db 84 AGQEQLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143
QY 121 KETLAFILNMGDHVTIRLDREWEPELNEAIPNDERDITTPVAMATTIRKLITGELLTLASRQ 180
Db 144 KETLAFILNMGDHVTIRLDREWEPELNEAIPNDERDITTPVAMATTIRKLITGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITIALGPDGKPSRIWIYTTG 240
Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITIALGPDGKPSRIWIYTTG 263
QY 241 SQATMDERNRQIAEIGASLIKHW 263
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 10
US-09-129-611-14
; Sequence 14, Application US/09129611A
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/129,611A
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33

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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-129-611-14

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Query Match	98.9%	Score 1330;	DB 15;	Length 286;
Best Local Similarity	98.9%;	Pred. No. 6e-132;		
Matches 260; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

QY	I HPETLVKRYDAEDOLGARVGYIELDINSGEILLESFRSEEREPWMSTEFKVLLCGAVLSRID	60
Dd	HPETLVKRYDAEDOLGARVGYIELDINSGEILLESFRSEEREPWMSTEFKVLLCGAVLSRID	83
QY	AGOEOLGRRIRHYSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNNTAANLLTTIGP	120
Dd	AGOEOLGRRIRHYSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNNTAANLLTTIGP	143
QY	KELTFAFLHMGDHVTRLDRWEPELNEAI PNDERDTTPVAMATTLRKLITGELLTLASRQ	180
Dd	KELTFAFLHMGDHVTRLDRWEPELNEAI PNDERDTTPVAMATTLRKLITGELLTLASRQ	203
QY	QLIDPMMEADKVAGPLLRSAIPAGMTIADKSGAGERGSRGIIAALGPDGKPSRIIVITYTG	240
Dd	QLIDPMMEADKVAGPLLRSAIPAGMTIADKSGAGERGSRGIIAALGPDGKPSRIIVITYTG	263
QY	SQA TMDERNRQIAEIGASLIKHW	263
Dd	SQA TMDERNRQIAEIGASLIKHW	286

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RESULT 11
US-09-129-611-21
; Sequence 21, Application US/09129611A
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/129,611A
; CURRENT FILING DATE: 1999-08-05
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-129-611-21

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	Query Match	98.9%;	Score 1330;	DB 15;	Length 286;	
	Best Local Similarity	98.9%;	Pred. No. 6e-132;			
	Matches 260;	Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;
QY	1 HPEITLVKVKDAEDQLGARVGIELDLSGEILSEFSERSEERPMMSTFKYLICGAVLSRID       	:				
Db	24 HPETLVKVKDAEDQLGARVGIIELDLNSGKILESREPRERFPMSTMTEKYLLCGAVLSRID 					
QY	61 AGQEQLGRRIHYSQNLDVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 					
Db	84 AGQEQLGRRIHYSQNLDVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 					
QY	121 KELLTAFLNMGDHVTRLDRWEPELNEAI PNDE RDTTTPVAMATTLRKLLTGELLTLASRQ 					
Db	144 KELTAFLNMGDHVTRLDRWEPELNEAI PNDE RDTTTPVAMATTLRKLTLGELLTLASRQ 					
QY	181 QILDWMEADKVAGPPLRSALPAGWF IADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 					
Db	204 QILDWMEADKVAGPPLRSALPAGWF IADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 					

QY	241	SOATMDERNQIAEIGASLIKHW	263
Db	264	SOATMDERNQIAEIGASLIKHW	286

```

RESULT 12
US-09-490-070-265
; Sequence 265, Application US/09490070
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
;      Pack, Peter
;      Ilag, Vic
;      Ge, Liming
;      Moroney, Simon
;      Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
;      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
;      STREET: 1251 Avenue of the Americas
;      CITY: New York
;      STATE: New York
;      COUNTRY: USA
;      ZIP: 10021
; COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/490,070
;      FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 09/025,769
;      FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
;      NAME: James F. Haley, Jr., Esq.
;      REGISTRATION NUMBER: 27,794
;      REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212)596-9000
;      TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 265:
; SEQUENCE CHARACTERISTICS:
;      LENGTH: 286 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:
US-09-490-070-265

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	Query Match	98.9%;	Score 1330;	DB 18;	Length 286;	
	Best Local Similarity	98.9%;	Pred. No. 6e-132;			
	Matches 260;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	1 HPE TLVKKDAEDQLGARVG YIELDLNSGELLESFRSEERFPMSTFKVLICGAVLSRID       :					60
Dd	24 HPETLVKVKDAEDQLGARVGIYELD LNSGKILSFRRPRRFPMTSTFKVLLCGAVLSRID 					83
QY	61 AGQEQLGRRIHYSQN DLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 					120
Dd	84 AGQEQLGRRIHYSQN DLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 					143
QY	121 KELLTAFLHNMGDHVTRLD RMEPELN EAI PNDERD TTPVAMATTLRKLLTGELLT LASRQ 					180
Dd	144 KELTAFLHNMGDHVTR LD RMEPELN EAI PNDERD TTPVAMATTLRKLLTGELLT LASRQ 					203
QY	181 QLIDWMEADKVAGPLIR SALLPAGWFIADKSGAGERGSRGIIALGPDGKPSRIIVITYTTG 					240
Dd	204 QLIDWMEADKVAGPL IR SALLPAGWFIADKSGAGERGSRGIIALGPDGKPSRIIVITYTTG 					263
QY	241 SQATMDERNRQIAETIGASLIKHW 					263

Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 13  
US-09-490-070-362

; Sequence 362, Application US/09490070

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

; STREET: 1251 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10021

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,070

; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/025,769

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: James F. Haley, Jr., Esq.

; REGISTRATION NUMBER: 27,794

; REFERENCE/DOCKET NUMBER: MORPHO/5

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)596-9000

; TELEFAX: (212)596-9090

; INFORMATION FOR SEQ ID NO: 362:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 286 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 362:

US-09-490-070-362

Query Match 98.9%; Score 1330; DB 18; Length 286;

Best Local Similarity 98.9%; Pred. No. 6e-132;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILSFRRSEERRPMMSTFKVLLCGAVLSRID 60

Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQIGRIIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120

Db 84 AGQEQIGRIIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143

QY 121 KELTAFHNMGDVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180

Db 144 KELTAFHNMGDVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203

QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITTTG 240

Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITTTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263

Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 14  
US-09-490-070A-265

; Sequence 265, Application US/09490070A

; GENERAL INFORMATION:

; APPLICANT: Knappik, Achim

; Pack, Peter

; Ilag, Vic

; Ge, Liming

; Moroney, Simon

; Plueckthun, Andreas

; TITLE OF INVENTION: Protein/(Poly)peptide libraries

; NUMBER OF SEQUENCES: 373

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

; STREET: 1666 K Street, N.W., Suite 300

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20006

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/490,070A

; FILING DATE: 24-Jan-2000

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95 11 3021.0

; FILING DATE: 18-AUG-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Colin G. Sandercock, Esq.

; REGISTRATION NUMBER: 31,298

; REFERENCE/DOCKET NUMBER: 37629-0005

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 912-2000

; TELEFAX: (202) 912-2020

; INFORMATION FOR SEQ ID NO: 265:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 286 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 265:

US-09-490-070A-265

Query Match 98.9%; Score 1330; DB 18; Length 286;

Best Local Similarity 98.9%; Pred. No. 6e-132;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILSFRRSEERRPMMSTFKVLLCGAVLSRID 60

Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQIGRIIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120

Db 84 AGQEQIGRIIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143

QY 121 KELTAFHNMGDVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180

Db 144 KELTAFHNMGDVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203

QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITTTG 240

Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITTTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263

Db 264 SQATMDERNRQIAEIGASLIKHW 286



Search completed: June 18, 2004, 19:13:52  
Job time : 185 secs

RESULT 15

US-09-490-070A-362

/ Sequence 362, Application US/09490070A

/ GENERAL INFORMATION:

/ APPLICANT: Knappik, Achim

/ Pack, Peter

/ Ilag, Vic

/ Ge, Liming

/ Moroney, Simon

/ Plueckthun, Andreas

/ TITLE OF INVENTION: Protein/(Poly)peptide libraries

/ NUMBER OF SEQUENCES: 373

/ CORRESPONDENCE ADDRESS:

/ ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman

/ White & McAniff

/ STREET: 1666 K Street, N.W., Suite 300

/ CITY: Washington

/ STATE: D.C.

/ COUNTRY: USA

/ ZIP: 20006

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/09/490,070A

/ FILING DATE: 24-Jan-2000

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: EP 95 11 3021.0

/ FILING DATE: 18-ADG-1995

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Colin G. Sandercock, Esq.

/ REGISTRATION NUMBER: 31,298

/ REFERENCE/DOCKET NUMBER: 37629-0005

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (202) 912-2000

/ TELEFAX: (202) 912-2020

/ INFORMATION FOR SEQ ID NO: 362:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 286 amino acids

/ TYPE: amino acid

/ TOPOLOGY: linear

/ MOLECULE TYPE: protein

/ SEQUENCE DESCRIPTION: SEQ ID NO: 362:

US-09-490-070A-362

Query Match 98.9%; Score 1330; DB 18; Length 286;

Best Local Similarity 98.9%; Pred. No. 6e-132;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	HPETLVKVKDAEDQLGARVGYIELDLNSGRIIESFRSEERFPMMSTFKVLLCGAVLSRID	60
Db	24	HPETLVKVKDAEDQLGARVGYIELDLNSGRIIESFRSEERFPMMSTFKVLLCGAVLSRID	83
QY	61	AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP	120
Db	84	AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP	143
QY	121	KELTAFLHNMGDHYTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELTLASRQ	180
Db	144	KELTAFLHNMGDHYTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELTLASRQ	203
QY	181	QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVIYTTG	240
Db	204	QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVIYTTG	263
QY	241	SOATMDERNROIAETIGASLIKH	263
Db	264	SOATMDERNROIAETIGASLIKH	286

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OM protein - protein search, using sw model

Run on: June 18, 2004, 18:30:18 ; Search time 18 Seconds

(without alignments)  
760.803 Million cell updates/sec

Title: EPPER526106.PEP

Perfect score: 1345

Sequence: 1 hpetlvkvkdaedqlgarvg.....tmdernrqiaiegaslikhw 263

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1325	98.5	286	1	BLAT_ECOLI
2	942	70.0	286	1	BLA1_ECOLI
3	940	69.9	286	1	BLI3_KLEPN
4	937	69.7	286	1	BLA8_ECOLI
5	936	69.6	286	1	BLA2_ECOLI
6	935	69.5	286	1	BLA2_ECOLI
7	933	69.4	286	1	BLA3_KLEPN
8	932	69.3	286	1	BLA5_KLEPN
9	929	69.1	265	1	BLA4_KLEPN
10	905	67.3	279	1	BLAC_KLEPN
11	879	65.4	269	1	BLA6_KLEPN
12	874	65.0	286	1	BLA1_ENTCL
13	672	50.0	298	1	BLAC_PROMI
14	573	42.6	304	1	BLA1_AERHY
15	539.5	40.1	288	1	BLC3_PSEAE
16	539.5	40.1	288	1	BLP4_PSEAE
17	536.5	39.9	288	1	BLC6_VIBCH
18	535.5	39.8	288	1	BLP1_PSEAE
19	516.5	38.4	290	1	BL02_KLEOX
20	513.5	38.2	291	1	BL01_KLEOX
21	512.5	38.1	293	1	BLAC_RHOCA
22	505.5	37.6	302	1	BLAC_NOCLA
23	498.5	37.1	288	1	BLC4_PSEAE
24	496.5	36.9	294	1	BLAC_YEREN
25	494.5	36.8	306	1	BLAC_STRFR
26	490	36.4	291	1	BLT1_ECOLI
27	489.5	36.4	305	1	BLA1_HAEIN
28	487	36.2	291	1	BLC2_SALTY
29	486.5	36.2	267	1	BLAC_SERFO
30	483.5	35.9	306	1	BLAC_BACSU
31	483	35.9	314	1	BLA2_STRCI
32	482.5	35.9	306	1	BLAC_BACAM
33	477	35.5	291	1	BLC1_ECOLI

34	476	35.4	303	1	BLA2_XANMA	P96465 xanthomonas
35	474	35.2	291	1	BLC3_SALTY	O33807 salmoneilla
36	471.5	35.1	294	1	BLAC_CITDI	P22390 citrobacter
37	471	35.0	291	1	BLC5_SALTY	O65975 salmoneilla
38	467.5	34.8	309	1	BLAC_BACTU	Q45726 bacillus th
39	467	34.7	291	1	BLC6_SALTY	O65976 salmoneilla
40	466.5	34.7	311	1	BLAC_STRCE	Q06650 streptomyc
41	462	34.3	325	1	BLA1_STRCI	Q03680 streptomyc
42	459.5	34.2	305	1	BLAC_STRIA	P35393 streptomyc
43	458.5	34.1	294	1	BLAF_MYCFO	Q59517 mycobacteri
44	456	33.9	306	1	BLAC_BACCE	P00809 bacillus ce
45	455.5	33.9	306	1	BLA1_BACMY	P28018 bacillus my

ALIGNMENTS

RESULT 1	ID	BLAT_ECOLI	STANDARD;	PRT;	286 AA.
AC	P00810; Q47313;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, last sequence update)				
DT	10-OCT-2003 (Rel. 42, last annotation update)				
DE	Beta-lactamase TEM precursor (EC 3.5.2.6) (TEM-1) (TEM-2) (TEM-3)				
DE	(TEM-4) (TEM-5) (TEM-6) (TEM-8/CAZ-2) (TEM-16/CAZ-7) (TEM-24/CAZ-6)				
DE	(IRT-4) (Penicillinase).				
GN	(BLA OR HCM1.216) AND BLAT-3 AND BLAT-4 AND BLAT-5 AND BLAT-6.				
OS	Escherichia coli, and				
OS	Salmonella typhi.				
OG	Plasmid R1 (R7268), Plasmid IncFII R100, Plasmid R6K, Plasmid pUD16,				
OG	Plasmid pCFE04, Plasmid pCFP14, and Plasmid pHCW1.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Escherichia.				
OX	NCBI_TaxID=562, 601;				
RN	[1]				
RP	SEQUENCE FROM N.A. (TEM-1).				
RC	SPECIES=E.coli; PLASMID=R1 (R7268); TRANSPOSON=Tn3;				
RX	MEDLINE=79012484; PubMed=358200;				
RA	Sutcliffe J.G.;				
RT	"Nucleotide sequence of the ampicillin resistance gene of Escherichia				
RT	coli plasmid pBR322."				
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3737-3741(1978).				
RN	[2]				
RP	SEQUENCE FROM N.A. (TEM-1).				
RC	SPECIES=E.coli; PLASMID=R1 (R7268); TRANSPOSON=Tn3;				
RX	MEDLINE=8002802; PubMed=383387;				
RA	Sutcliffe J.G.;				
RT	"Complete nucleotide sequence of the Escherichia coli plasmid				
RT	pBR322."				
RL	Cold Spring Harb. Symp. Quant. Biol. 43:77-90(1979).				
RN	[3]				
RP	SEQUENCE FROM N.A. (TEM-1).				
RC	PLASMID=IncFII R100;				
RX	MEDLINE=86319522; PubMed=3019092;				
RA	Ohtsubo H., Ryder T.B., Maeda Y., Armstrong K., Ohtsubo E.;				
RT	"DNA replication of the resistance plasmid R100 and its control."				
RL	Adv. Biophys. 21:115-133(1986).				
RN	[4]				
RP	SEQUENCE OF 24-286 (TEM-2).				
RC	SPECIES=E.coli; PLASMID=R6K; TRANSPOSON=Tn1;				
RX	MEDLINE=79012483; PubMed=358199;				
RA	Ambler R.P., Scott G.K.;				
RT	"Partial amino acid sequence of penicillinase coded by Escherichia				
RT	coli plasmid R6K."				
RL	Proc. Natl. Acad. Sci. U.S.A. 75:3732-3736(1978).				
RN	[5]				
RP	SEQUENCE FROM N.A. (TEM-3).				
RC	Sougakoff W., Goussard S., Courvalin P.;				
RA	"The TEM-3 beta-lactamase, which hydrolyzes broad-spectrum				
RT	cephalosporins, is derived from the TEM-2 penicillinase by two amino				
RT	acid substitutions."				
RL	FEMS Microbiol. Lett. 56:343-348(1988).				

RN [6]  
 RP SEQUENCE FROM N.A. (TEM-3).  
 RC PLASMID=PCFF04;  
 RX MEDLINE=93062798; PubMed=1331747;  
 RA Mabilat C., Lourencao-Vital J., Goussard S., Courvalin P.;  
 RT "A new example of physical linkage between *tnl* and *tnz1*: the  
 RN antibiotic multiple-resistance region of plasmid PCFF04 encoding  
 RT extended-spectrum beta-lactamase TEM-3.";  
 RL Mol. Genet. 235:113-121(1992).  
 RN [7]  
 RP SEQUENCE FROM N.A. (TEM-4 AND TEM-5).  
 RC STRAIN=CB86134; PLASMID=pud16, and pCFF04;  
 RX MEDLINE=89378760; PubMed=2550326;  
 RA Sougakoff W., Petit A., Goussard S., Sirot D., Bure A., Courvalin P.;  
 RT "Characterization of the plasmid genes *blaT-4* and *blaT-5* which encode  
 RT the broad-spectrum beta-lactamases TEM-4 and TEM-5 in  
 RT enterobacteriaceae.";  
 RL Gene 78:339-348(1989).  
 RN [8]  
 RP SEQUENCE FROM N.A. (TEM-6).  
 RC STRAIN=HB251;  
 RX MEDLINE=92166702; PubMed=1665171;  
 RA Goussard S., Sougakoff W., Mabilat C., Bauernfeind A., Courvalin P.;  
 RT "An ISI-like element is responsible for high-level synthesis of  
 RT extended-spectrum beta-lactamase TEM-6 in Enterobacteriaceae.";  
 RL J. Gen. Microbiol. 137:2681-2687(1991).  
 RN [9]  
 RP SEQUENCE FROM N.A. (TEM-8; TEM-16 AND TEM-24).  
 RX MEDLINE=93037315; PubMed=1416873;  
 RA Chanal C., Poupart M.C., Sirot D., Labia R., Sirot J., Cluzel R.;  
 RT "Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase  
 RT genes.";  
 RL Antimicrob. Agents Chemother. 36:1817-1820(1992).  
 RN [10]  
 RP SEQUENCE OF 24-286 (IRT-4).  
 RC STRAIN=PEY;  
 RX MEDLINE=94333751; PubMed=8056282;  
 RA Brun T., Peduzzi J., Canica M.M., Paul G., Nevot P., Barthelmy M.,  
 RA Labia R.;  
 RT "Characterization and amino acid sequence of IRT-4, a novel TEM-type  
 RT enzyme with a decreased susceptibility to beta-lactamase  
 RT inhibitors.";  
 RL FEMS Microbiol. Lett. 120:111-117(1994).  
 RN [11]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=S.typhi; STRAIN=CT18; PLASMID=pHCM1;  
 RX MEDLINE=21534947; PubMed=11677608;  
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,  
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahinia M.,  
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,  
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,  
 RA Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,  
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,  
 RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,  
 RA Whitehead S., Barrell B.G.;  
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*  
 RT enterica serovar Typhi CT18.";  
 RL Nature 413:848-852(2001).  
 RN [12]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF TEM-1.  
 RX MEDLINE=92183921; PubMed=1544485;  
 RA Jelsch C., Lenfant F., Masson J.-M., Samama J.-P.;  
 RT "Beta-lactamase TEM1 of *E. coli*. Crystal structure determination at  
 RT 2.5-A resolution.";  
 RL FEBS Lett. 299:135-142(1992).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF TEM-1.  
 RX MEDLINE=93361453; PubMed=8356032;  
 RA Jelsch C., Mourey L., Masson J.-M., Samama J.-P.;  
 RT "Crystal structure of *Escherichia coli* TEM1 beta-lactamase at 1.8-A  
 RT resolution.";  
 RL Proteins 16:364-383(1993).  
 RN [14]

RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF TEM-1 COMPLEXED WITH BLIP.  
 RX MEDLINE=96186252; PubMed=8605632;  
 RA Strynadka N.C.J., Jensen S.E., Alzari P.M., James M.N.G.;  
 RT "A potent new mode of beta-lactamase inhibition revealed by the 1.7 A  
 RT X-ray crystallographic structure of the TEM-1-BLIP complex.";  
 RL Nat. Struct. Biol. 3:290-297(1996).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF TEM-1.  
 RX MEDLINE=98153145; PubMed=9485412;  
 RA Maveyraud L., Pratt R.F., Samama J.-P.;  
 RT "Crystal structure of an acylation transition-state analog of the  
 RT TEM-1 beta-lactamase. Mechanistic implications for class A beta-  
 RT lactamases.";  
 RL Biochemistry 37:2622-2628(1998).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (2.28 ANGSTROMS) OF TEM-1.  
 RX MEDLINE=99352177; PubMed=10423234;  
 RA Swaren P., Golemi D., Cabantous S., Bulchev A., Maveyraud L.,  
 RA Mobashery S., Samama J.-P.;  
 RT "X-ray structure of the Asn276Asp variant of the *Escherichia coli*  
 RT TEM-1 beta-lactamase: direct observation of electrostatic modulation  
 RT in resistance to inactivation by clavulanic acid.";  
 RL Biochemistry 38:9570-9576(1999).  
 CC -!- FUNCTION: TEM-type are the most prevalent beta-lactamases in  
 CC enterobacteria; they hydrolyze the beta-lactam bond in susceptible  
 CC beta-lactam antibiotics, thus conferring resistance to penicillins  
 CC and cephalosporins. TEM-3 and TEM-4 are capable of hydrolyzing  
 CC cefotaxime and ceftazidime. TEM-5 is capable of hydrolyzing  
 CC ceftazidime. TEM-6 is capable of hydrolyzing ceftazidime and  
 CC aztreonam. TEM-8/CAZ-2, TEM-16/CAZ-7 and TEM-24/CAZ-6 are markedly  
 CC active against ceftazidime. IRT-4 shows resistance to beta-  
 CC lactamase inhibitors.  
 CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
 CC amino acid.  
 CC -!- BIOTECHNOLOGY: This protein is used as a marker in many commonly  
 CC used cloning vectors, such as pBR322 and the pUC series.  
 CC -!- MISCELLANEOUS: The beta-lactamase present on pBR322 was cloned  
 CC from plasmid R1 (R7268).  
 CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.  
 CC -----  
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 CC -----  
 DR EMBL; J01749; BAB59737.1; -.  
 DR EMBL; V00613; CAA23886.1; -.  
 DR EMBL; X64523; CAA45828.1; -.  
 DR EMBL; X57972; CAA41038.1; -.  
 DR EMBL; X65252; CAA46344.1; -.  
 DR EMBL; X65253; CAA46345.1; -.  
 DR EMBL; X65254; CAA46346.1; -.  
 DR EMBL; U89928; AAB64386.1; -.  
 DR EMBL; U66885; AAC48875.1; -.  
 DR EMBL; AL513383; CAD09800.1; -.  
 DR PIR; A93821; PNECP.  
 DR PIR; S30113; S30113.  
 DR PDB; 1BTU; 26-JAN-95.  
 DR PDB; 1TEM; 15-MAY-97.  
 DR PDB; 1XPB; 01-APR-97.  
 DR PDB; 1AXB; 18-NOV-98.  
 DR PDB; 1CK3; 18-AUG-99.  
 DR PDB; 1BT5; 02-SEP-99.  
 DR PDB; 1ERM; 20-DEC-00.  
 DR PDB; 1ERO; 20-DEC-00.  
 DR PDB; 1ERO; 20-DEC-00.  
 DR PDB; 1ESU; 03-MAY-00.  
 DR PDB; 1FOG; 01-NOV-00.  
 DR PDB; 1JTD; 18-DEC-02.  
 DR PDB; 1JTG; 17-OCT-01.

Query Match 98.5%; Score 1325; DB 1; Length 286;  
 Best Local Similarity 98.1%; Pred. No. 6.6e-98;  
 Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVKVKADQDQLGARVGIYELDLSNGSILESFRSEERFPMMSTFKVLLCGAVISRID 60  
 Db 24 HPETLVKVKADQDQLGARVGIYELDLSNGSILESFRSEERFPMMSTFKVLLCGAVISRVD 83  
 QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
 Db 84 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
 QY 121 KELTAFLEHNGDHTVRLDRWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
 Db 144 KELTAFLEHNGDHTVRLDRWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
 QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSGRII AALGPDGKPSRIYIYTTG 240  
 Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSGRII AALGPDGKPSRIYIYTTG 263  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 2  
 BLAI\_ECOLI STANDARD; PRT; 286 AA.  
 AC P14557; 007941; P23982;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Beta-lactamase SHV-1 precursor (EC 3.5.2.6) (PIT-2).  
 GN BLA OR SHV1.  
 OS Escherichia coli, and  
 OS Klebsiella pneumoniae.  
 OG Plasmid R974, and Plasmid p453.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562, 573;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=K.pneumoniae; PLASMID=R974;  
 RX MEDLINE=91024126; PubMed=2221867;  
 RA Mercier J., Levesque R.C.;  
 RT "Cloning of SHV-2, OHIO-1, and OXA-6 beta-lactamases and cloning and  
 sequencing of SHV-1 beta-lactamase.";  
 RL Antimicrob. Agents Chemother. 34:1577-1583(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=K.pneumoniae; STRAIN=KPAA-1, KPZU-8, and KPZU-13;  
 RX MEDLINE=97291235; PubMed=9145849;  
 RA Nuesch-Inderbinen M., Kayser F.H., Hachler H.;  
 RT "Survey and molecular genetics of SHV beta-lactamases in  
 Enterobacteriaceae in Switzerland: two novel enzymes, SHV-11 and SHV-  
 12.";  
 RL Antimicrob. Agents Chemother. 41:943-949(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=K.pneumoniae; STRAIN=15571;  
 RX Rice L.B., Bonafede M., Hujer A.M., Bonomo R.A.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=E.coli; STRAIN=HB101;  
 RA Bradford P.A.;  
 RT "Automated thermal cycling is superior to traditional methods for  
 nucleotide sequencing of blashv genes.";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 22-286.  
 RC SPECIES=E.coli; PLASMID=p453;

RX MEDLINE=88268817; PubMed=3260490;  
 RA Barthelemy M., Peduzzi J., Labia R.;  
 RT "Complete amino acid sequence of p453-plasmid-mediated PIT-2 beta-  
 lactamase (SHV-1).";  
 RL Biochem. J. 251:73-79(1988).  
 RN [6]  
 RP SEQUENCE OF 22-128.  
 RC SPECIES=E.coli; PLASMID=p453;  
 RX MEDLINE=87279638; PubMed=3497152;  
 RA Barthelemy M., Peduzzi J., Labia R.;  
 RT "N-terminal amino acid sequence of PIT-2 beta-lactamase (SHV-1).";  
 RL J. Antimicrob. Chemother. 19:839-841(1987).  
 RN [7]  
 RP X-RAY CRYSTALLOGRAPHY (1.98 ANGSTROMS).  
 RC SPECIES=K.pneumoniae; STRAIN=15571;  
 RX MEDLINE=99249781; PubMed=10231522;  
 RA Kuzin A.P., Nukaga M., Nukaga Y., Hujer A.M., Bonomo R.A., Knox J.R.;  
 RT "Structure of the SHV-1 beta-lactamase.";  
 RL Biochemistry 38:5720-5727(1999).  
 CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
 amino acid.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY. DIFFERS  
 IN ONLY ONE POSITION FROM SHV-2.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; M59181; AAA26087.1; -;  
 DR EMBL; X98098; CAA66726.1; -;  
 DR EMBL; X98099; CAA66727.1; -;  
 DR EMBL; X98100; CAA66728.1; -;  
 DR EMBL; AF124984; AAD18054.1; -;  
 DR EMBL; AF148850; AAD37412.1; -;  
 DR PIR; A44996; A44996.  
 DR PDB; 1SHV; 05-MAY-99.  
 DR PDB; 1G56; 14-FEB-01.  
 DR InterPro; IPR001466; Beta\_lactamase.  
 DR InterPro; IPR000871; Beta\_lactamase\_A.  
 DR Pfam; PF00144; beta-lactamase; 1.  
 DR PRINTS; PR00118; BLACTAMASEA.  
 DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
 KW Hydroxylase; Antibiotic resistance; Plasmid; signal; 3D-structure.  
 FT SIGNAL 1 21  
 FT CHAIN 22 286 BETA-LACTAMASE SHV-1.  
 FT ACT\_SITE 66 66  
 FT DISULFID 73 119  
 FT BINDING 230 232  
 FT CONFLICT 112 112  
 FT CONFLICT 136 137  
 FT CONFLICT 188 189  
 FT CONFLICT 278 278  
 FT CONFLICT 281 281  
 FT HELIX 25 36  
 FT TURN 37 37  
 FT STRAND 39 46  
 FT TURN 47 49  
 FT STRAND 52 56  
 FT TURN 58 59  
 FT STRAND 62 63  
 FT HELIX 65 67  
 FT HELIX 68 81  
 FT TURN 82 83  
 FT TURN 87 88  
 FT STRAND 90 91  
 FT HELIX 95 97  
 FT TURN 103 104  
 FT HELIX 105 108  
 FT TURN 109 111

SUBSTRATE (BY SIMILARITY).  
 G -> A (IN REF. 1).  
 AT -> TA (IN REF. 5).  
 KL -> NVG (IN REF. 1).  
 A -> K (IN REF. 1).  
 I -> Y (IN REF. 1).

FT	STRAND	113	114	
FT	HELIX	115	124	
FT	HELIX	128	137	
FT	TURN	138	139	
FT	HELIX	140	150	
FT	TURN	151	152	
FT	STRAND	157	157	
FT	TURN	162	163	
FT	HELIX	164	166	
FT	TURN	170	171	
FT	TURN	174	175	
FT	STRAND	176	177	
FT	HELIX	179	191	
FT	TURN	193	194	
FT	HELIX	197	208	
FT	TURN	209	209	
FT	HELIX	214	220	
FT	TURN	223	224	
FT	STRAND	226	233	
FT	TURN	236	237	
FT	STRAND	239	246	
FT	TURN	248	249	
FT	STRAND	253	260	
FT	HELIX	266	282	
FT	TURN	283	283	
SQ	SEQUENCE	286 AA;	31224 MW;	C78F42667E698E6C CRC64;

Query Match	70.0%;	Score 942;	DB 1;	Length 286;
Best Local Similarity	68.3%;	Pred. No. 1.5e-67;		
Matches 179;	Conservative 38;	Mismatches 45;	Indels 0;	Gaps 0;

QY	2	PETLVKVCDAEDQLGARVGIYELDINSGEILSEFRSEERFPMWSTFKVLLCGAVLSRIDA	61
		: : : :   :   :   :   :   : : : :   : : : :   : : : :	
Db	23	POPLFQIKLISESQLSGRVGMIEMLDASGRLLTAWRADERFPMWSTFKVLLCGAVLARVA	82
QY	62	GOEQLGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGBPK	121
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	83	GDEQLERKIHRYQODLVDPSPVSEKHLADGMTVGELECAAAITMSDNSAANLLLATVGPA	142
QY	122	ELTAFLHNMGDHYTRLDRWEPELNEALPENDERDTTTPVAMATTLRKLITGELLTLASRQ	181
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	143	GLTAFLRQIGDNVTRLRDMETELNEALPGDARDTTTPASMAATTLRKLITTSQRLSARSQ	202
QY	182	LIDWMEADKVAGPBLRSALPAGWFIADKSGAGERSGRIIAALGPDGKPSRIVVIYTTGS	241
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	203	LLOQWVDDRVAGPLIRSVLPAGWFIADKSGAGERGARGIIVALLGPNKKAERIVVIYLTDT	262
QY	242	QATMDERNRQIAETGASLIKHW	263
		:   :   :   :   :   :   :   :   :   :   :   :   :   :   :	
Db	263	PASMAERNQOAGIGALLIEHW	284

```

RESULT 3
BL13_KLEPN
ID BL13 KLEPN STANDARD; PRT; 286 AA.
AC Q9S424;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Beta-lactamase SHV-13 precursor (EC 3.5.2.6).
GN BLA OR SHV13.
OS Klebsiella pneumoniae.
OG Plasmid.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=803;
RX MEDLINE=20187177; PubMed=10722518;
RA Yuan M., Hall J.M.C., Savelkoul P.H.M., Vandenbroucke-Grauls C.M.J.E.,
RA Livermore D.M.;
RT "SHV-13, a novel extended-spectrum beta-lactamase, in Klebsiella

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RT pneumoniae isolates from patients in an intensive care unit in
RT Amsterdam.";
RL Antimicrob. Agents Chemother. 44:1081-1084 (2000).
CC -1- FUNCTION: Broad spectrum beta-lactamase which hydrolyzes
CC penicillins, as well as cephalosporins except cephamycins. Also
CC hydrolyzes aztreonam, but not imipenem. Confers highly resistance
CC to ceftazidime, cefotaxime, aztreonam and piperacillin.
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -1- ENZYME REGULATION: Inhibited 16-fold better by the beta-lactamase
CC inhibitor clavulanic acid than by tazobactam.
CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.
CC -----
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DR	EMBL; AF164577; AAD43815.1; -.
DR	HSSP; P14557; 1SHV.
DR	InterPro; IPR001466; Beta_lactamase.
DR	InterPro; IPR000871; Beta_lactamase_A.
DR	Pfam; PF00144; beta-lactamase; 1.
DR	PRINTS; PR00118; B1ACTAMASEA.
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW	Hydrolase; Antibiotic resistance; Signal; Plasmid.
FT	SIGNAL 1 21 POTENTIAL.
FT	CHAIN 22 286 BETA-LACTAMASE SHV-13.
FT	ACT_SITE 66 66 BY SIMILARITY.
FT	DISULFID 73 119 BY SIMILARITY.
FT	BINDING 230 232 SUBSTRATE (BY SIMILARITY).
SO	SEQUENCE 286 AA; 31253 MW; CBBF426DA3FF5502 CRC64;

Query Match	69.9%;	Score 940;	DB 1;	Length 286;
Best Local Similarity	67.9%;	Pred. No. 2.1e-67;		
Matches 178; Conservative	38;	Mismatches 46;	Indels 0;	Gaps 0

QY		2	PETLVKKDAEDOLGARVGVIELDLNNGELLESEFRSEERFPMSTFKVLICGAVLSRIDA	61
Dd		23	POPLEQIKQESQLSGRVGMIEMDLASGRTITAMRADERFPMMSTFKVILCGAVLARVDA	82
QY		62	GQEOLGRRIHYSQNDELVEYSPVTEKHLTDGMTVELCSAAITMSDNTAANLLTTIGGPX	121
Dd		83	GDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVELCAAATMSDNSAANLLLATVGDPA	142
QY		122	ELTAFLEHNMGDVTRLDRWPELNEAIPNDERDTTPPVAMATTLRKLITGELLTLASROO	181
Dd		143	GLTAFLRLQIGDNVTRLDRMWETELNEALPGDARDTTPPASMATLRKLITSORLSARSORO	202
QY		182	LIDMMEADKYAGPLLRSALLPWGFIADKSGAGEGSRGITTAALGPDGKPSRIIVITYTGS	241
Dd		203	LLQNMWDDRYVAGPLIRSVLPAGWFIADKTGAEARGARGIIVALLGPNNKAERIIVIYLRT	262
QY		242	OATMDERNQJLAETIGASLIKHM	263
Dd		263	PASMAERNQJLAGIGAALIEMH	284

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RESULT 4
BLA8_ECOLI
ID      BLA8_ECOLI      STANDARD;      PRT;      286 AA.
AC      008337;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Beta-lactamase SHV-8 precursor (EC 3.5.2.6).
GN      BLA OR SHV8.
OS      Escherichia coli.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.

```

OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97209066; PubMed=9056008;  
 RA Rashed J.K., Jay C., Metchock B., Berkowitz F., Weigel L.,  
 RA Crellin J., Steward C., Hill B., Medeiros A.A., Tenover F.C.;  
 RT "Evolution of extended-spectrum beta-lactam resistance (SHV-8) in a  
 RL strain of *Escherichia coli* during multiple episodes of bacteremia."; Antimicrob. Agents Chemother. 41:647-653(1997).  
 CC -! FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS  
 CC NOTABLY CEFOTAXIME AND CEFOTAZIDIME.  
 CC -! CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
 CC amino acid.  
 CC -! SIMILARITY: Belongs to the class-A beta-lactamase family.  
 CC -----  
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DR	EMBL; U92041; AAB51384.1; -.
DR	HSSP; P14557; 1SHV.
DR	InterPro; IPR001466; Beta_lactamase.
DR	InterPro; IPR000871; Beta_lactamase_A.
DR	Pfam; PF00144; beta-lactamase; 1.
DR	PRINTS; PR00118; BLACTAMASEA.
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KM	Hydrolase; Antibiotic resistance; signal.
FT	SIGNAL 1 21 POTENTIAL.
FT	CHAIN 22 286 BETA-LACTAMASE SHV-8.
FT	ACT_SITE 66 66 BY SIMILARITY.
FT	DISULFID 73 119 BY SIMILARITY.
FT	BINDING 230 232 SUBSTRATE (BY SIMILARITY).
SQ	SEQUENCE 286 AA; 31223 MW; F159990BC8BF5504 CRC64; .

Query Match 69.7%; Score 937; DB 1; length 286;  
Best Local Similarity 67.9%; Pred. No. 3.7e-67;  
Matches 178; Conservative 39; Mismatches 45; Indels 0; Gaps 0;

QY	2	PETLVKKDAEDOLGARVGIEIDLNSGEILSFSEERFEMMSTFKVLLCGAVLSRIDA	61
Dp	23	POPLEBOIKLSESQLSGRVGMIEMDLASGRTLLTAWRADEREFMMSTFKVLLCGAVLARVDA	82
QY	62	GQEOIGRRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTGGPK	121
Dp	83	GDEQOERKIHRYRQODLVDSFVSEKHLADGMTVGELCAAAITMSDNSAANLLTAIVGPA	142
QY	122	ELTAFLHNMGDHTRLDRWEPELNEALPNDERDITTPVAMATTLRKLITGELLTLASRQ	181
Dp	143	GLTAFLRQIGDNVTRLDRWETELNEALPGDARNTTTPASMAATLRKLITSQRLSARSQ	202
QY	182	LIDMWEADKVAAGPLLRSLPACWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITGTS	241
Dp	203	LLOMWYDVRVAGPLIRSVLPAGWFIADKTGAGERGARGIIVALLGPNNKAERIVVITLDT	262
QY	242	QATMDERNRQIAEIGASLIKHW	263
Dp	263	PASMAERNQOIAGIGAALIEHW	284

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RESULT 5
BLA2_ECOLI
ID      BLA2_ECOLI      STANDARD;      PRT;      286 AA.
AC
PI4558;
DT      01-JAN-1990 (Rel. 13, Created)
DT      01-MAY-1991 (Rel. 18, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Beta-lactamase SHV-2 precursor (EC 3.5.2.6) (SHV-2A)
GN      BLA OR SHV2.
OS      Escherichia coli,

```

OS *Klebsiella pneumoniae*,  
OS *Klebsiella pneumoniae* (subsp. *ozaenae*), and  
OS *Salmonella typhimurium*.  
OG Plasmid pBMH77, Plasmid pZMPL, Plasmid pBP60-1, and Plasmid pHT1.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562, 573, 574, 602;  
RN [1]  
RP SEQUENCE OF 22-286.  
RC SPECIES=E.coli; STRAIN=A2302; PLASMID=pBMH77;  
RX MEDLINE=88196385; PubMed=3129309;  
RA Barthelemy M., Peduzzi J., Yaghlane H.B., Labia R.;  
RT "Single amino acid substitution between SHV-1 beta-lactamase and  
RT cefotaxime-hydrolyzing SHV-2 enzyme.";   
RL FEBS Lett. 231:217-220(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=K.pneumoniae;  
RX MEDLINE=90264317; PubMed=2160941;  
RA lee K.Y., Hopkins J.D., Syvanen M.;  
RT "Direct involvement of IS26 in an antibiotic resistance operon.";   
RL J. Bacteriol. 172:3229-3236(1990).

RN SEQUENCE FROM N.A.  
 RP [5]  
 RC SPECIES=K.pneumoniae; STRAIN=KPR 14; PLASMID=pZMP1;  
 RX MEDLINE=91237320; PubMed=2033379;  
 RA Podbielski A., Schoenling J., Melzer B., Warnatz K., Leusch H.G.;  
 RT "Molecular characterization of a new plasmid-encoded SHV-type beta-  
 RT lactamase (SHV-2 variant) conferring high-level cefotaxime resistance  
 RT upon *Klebsiella pneumoniae*."; [5]  
 RL J. Gen. Microbiol. 137:569-578(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=K.pneumoniae; STRAIN=KPZU-3;  
 RX MEDLINE=96100740; PubMed=7486909;  
 RA Nuesch-Inderbinen M., Hachler H., Kayser F.H.;  
 RT "New system based on site-directed mutagenesis for highly accurate  
 RT comparison of resistance levels conferred by SHV beta-lactamases."; [5]  
 RL Antimicrob. Agents Chemother. 39:1726-1730(1995).  
 RN [5]

RP SEQUENCE FROM N.A.  
RC SPECIES=K.pneumoniae; STRAIN=KPLA-10;  
RX MEDLINE=97291235; PubMed=9145849;  
RA Nuesch-Inderbinen M., Kayser F.H., Hachler H.;  
RT "Survey and molecular genetics of SHV beta-lactamases in  
RT Enterobacteriaceae in Switzerland: two novel enzymes, SHV-11 and  
RT SHV-12. ";  
RL Antimicrob. Agents Chemother. 41:943-949(1997).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC SPECIES=K.ozanae; STRAIN=2180;  
RX MEDLINE=90370479; PubMed=2395654;  
RA Podbielski A., Melzer B.;  
RT "Nucleotide sequence of the gene encoding the SHV-2 beta-lactamase  
RT (blaSHV-2) of Klebsiella ozanae. ";  
RL Nucleic Acids Res. 18:4916-4916(1990).

RP SEQUENCE FROM N.A.  
RC PLASMID=DBP60-1;  
RX MEDLINE=91136192; PubMed=2285285;  
RA Huletsky A., Couture F., Levesque R.C.;  
RT "Nucleotide sequence and phylogeny of SHV-2 beta-lactamase.";  
RL Antimicrob. Agents Chemother. 34:1725-1732(1990).  
RN [8]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S.typhimurium; PLASMID=pHT1;  
RX MEDLINE=90351141; PubMed=2201259;  
RA Garbarg-Chenon A., Godard V., Labia R., Nicolas J.C.;  
RT "Nucleotide sequence of SHV-2 beta-lactamase gene.";  
RL Antimicrob. Agents Chemother. 34:1444-1446(1990).  
RN [9]  
RP SEQUENCE FROM N.A.  
RC SPECIES=E.coli; STRAIN=JC2926;  
RX

```

RN      [9]
RP      SEQUENCE FROM N.A.
RC      SPECIES=E.coli; STRAIN=JC2926;

```



```

RA  Bradford P.A.;
RT  "Automated thermal cycling is superior to traditional methods for
RT  nucleotide sequencing of blashv genes.";
RL  Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC
CC  -!- FUNCTION: This enzyme hydrolyzes cefotaxime, ceftazidime and other
CC  broad spectrum cephalosporins.
CC  -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC  amino acid.
CC  -!- SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY. DIFFERS
CC  IN ONLY ONE POSITION FROM SHV-1.
CC  -----
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CC	----
DR	EMBL; X62115; CAA44025.1; -.
DR	EMBL; X53433; CAA37524.1; -.
DR	EMBL; X53817; CAA37813.1; -.
DR	EMBL; X84314; CAA59058.1; -.
DR	EMBL; M95179; AAA25526.1; -.
DR	EMBL; I47119; AAA75015.1; -.
DR	EMBL; X98102; CAA66730.1; -.
DR	EMBL; AF148851; AAD37413.1; -.
DR	PIR; A44998; A44998.
DR	HSSP; P14557; 1SHV.
DR	InterPro; IPR001466; Beta_lactamase.
DR	InterPro; IPR000871; Beta_lactamase_A.
DR	Pfam; PF00144; beta-lactamase; 1.
DR	PRINTS; PR00118; BLACTAMASEA.
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW	Hydrolase; Antibiotic resistance; Plasmid; signal.
FT	SIGNAL 1 21
FT	CHAIN 22 286 BETA-LACTAMASE SHV-2.
FT	ACT_SITE 66 66 BY SIMILARITY.
FT	DISTEFLD 73 119 BY SIMILARITY.
FT	BINDING 230 232 SUBSTRATE (BY SIMILARITY).
FT	VARIANT 31 31 L -> Q (IN SHV-2A).
SEQ	SEQUENCE 286 AA; 31254 MW; 738F426651F551A CRC64;

Query Match	69.6%;	Score 936;	DB 1;	Length 286;
Best Local Similarity	67.9%;	Pred. No. 4.4e-67;		
Matches 178; Conservative	38;	Mismatches 46;	Indels 0;	Gaps 0;

QY	2	PETIVKVKDAEDOLGARVGYIELDLSNGELLESFRSEERFPMSTFEKVLICGAVLSRIDA	61
Db	23	PQPLEQIKLSESQLSGRVGMIEMDLASGRLLTAWRADERFPMSTFEKVVLCGAVLARVDA	82
QY	62	GQEQLRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLITIGPK	121
Db	83	GDEQERKTHYRQODLVDSFVSEKHLADGMTVGE LCAAAITMSDNSAANLLLATVGGPA	142
QY	122	ELTAFIHNMGDHYTRLDRWEPELNEAIPNDERDITTPVAMATTLRLKLTGELLTLASRQO	181
Db	143	GLTAFILRQIGDNVTRLDRMETELNEALPGDARDITTPASMAATTLRLKLTSGRLSARSQOQ	202
QY	182	LIDPMHEADKVAGPLLRSA LPAWGFIADKSGAGERSGIIAALGPDGKPSRIVIYTTGS	241
Db	203	LLOMMVDDRVAGPLIRSVLPAGWFIADKTSASERGARGIVALLGPNNKAERIVIYLRDT	262
QY	242	QATMDERNROIAEIGASLIIKHW	263
Db	263	PASMAERNQOITAGIGAAIIHWW	284

RESULT 6	
BL24_ECOLI	
ID BL24 ECOLI	STANDARD;
AC Q9S169;	PRT;
DT 16-OCT-2001	286 AA.
	(Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, last sequence update)  
DT 16-OCT-2001 (Rel. 40, last annotation update)  
DE Beta-lactamase SHV-24 precursor (EC 3.5.2.6).  
GN BLA OR SHV24.  
OS *Escherichia coli*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;

```

RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=HKY741;
RA      Kurokawa H., Yagi T., Shibata N., Arakawa Y.;
RT      "New SHV-derived extended-spectrum beta-lactamase gene.";
RL      Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS
CC      NOTABLY CEFOTAXIME AND CEFALAZIDIME.
CC      -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC      amino acid.
CC      -1- SIMILARITY: Belongs to the class-A beta-lactamase family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).

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CC	-----	
DR	EMBL; AB023477; BAA84973.1; -.	
DR	HSSP; P14557; 1SHV.	
DR	InterPro; IPR001466; Beta_lactamase.	
DR	InterPro; IPR000871; Beta_lactamase_A.	
DR	pfam; PF00144; beta_lactamase; 1.	
DR	PRINTS; PR00118; BLACTAMASEA.	
DR	PROSITE; PS00146; BETA_LACTAMASE_A; 1.	
KW	Hydrolase; Antibiotic resistance; Signal.	
FT	SIGNAL	1 21
FT	CHAIN	22 286
FT	ACT_SITE	66 66
FT	DISULFID	73 119
FT	BINDING	230 232
SQ	SEQUENCE	286 AA; 31166 MW; 5EA990BC8B0AAFF CRC64;

Query Match	69.5%;	Score 935;	DB 1;	Length 286;
Best Local Similarity	67.9%;	Pred. No. 5.3e-67;		
Matches 178; Conservative	38;	Mismatches 46;	Indels 0;	Gaps 0;

QY		2	PETLVKVKDAEDQLGARVGYIELDLNSGEILLESFRSEERFPMSTFKVLTCGAVLSRIDA	61
Dd		23	PQPLEQIKLSIESQLSGRVGMIEMLDLAGRTLTAWRADEREFPMMSTFKVVLTCGAVLARVDA	82
QY		62	GGEQIGRRIRHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGPK	121
Dd		83	GDEQEERKKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLATVGGPA	142
QY		122	ELEAFINMGDVHTRLDRWEPELNEALPNDERDTTPVAMATTIRKLITGELLTIASRQ	181
Dd		143	GLTAEFLRQIDGNVTRLDRWETELNEALPGDARGTTTPASMAATLRKLITSQRLSARSQRQ	202
QY		182	LIDMMEADKVAGPLLRSALPWGFIAADKSAGERGSRGTIAALGPDGKPSRIVIYTTGS	241
Dd		203	LLOVMVDDRVAGPLIRSVLPAGWFIADKTGAERGARGIVALLGPNNKAERTIVIIYLRDT	262
QY		242	QATMDERNROI AEIGASLIKH W	263
Dd		263	PASMAERNQOIAGIGAALI EHW	284

RESULT 7		
BLA3_KLEPN		
ID _BLA3_KLEPN	STANDARD;	PRT; 286 AA.
AC P30836;		
DT 01-JUL-1993	(Rel. 26, Created)	

01-JUL-1993 (Rel. 26, last sequence update)  
DT 10-OCT-2003 (Rel. 42, last annotation update)  
DE Beta-lactamase SHV-3 precursor (EC 3.5.2.6).  
GN BLA OR SHV3.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90146253; PubMed=2694951;  
RA Nicolas M.H., Jarlier V., Honore N., Philippon A., Cole S.T.;  
RT "Molecular characterization of the gene encoding SHV-3 beta-lactamase  
RT responsible for transferable cefotaxime resistance in clinical  
RT isolates of Klebsiella pneumoniae."  
RL Antimicrob. Agents Chemother. 33:2096-2100 (1989).  
CC -!- FUNCTION: This enzyme hydrolyzes cefotaxime, ceftazidime and other  
CC broad spectrum cephalosporins.  
CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
CC amino acid.  
CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.  
DR PIR; A37200; A37200.  
DR HSSP; P14557; ISHV.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
KW Hydrolase; Antibiotic resistance; Plasmid; Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 286 BETA-LACTAMASE SHV-3.  
FT ACT\_SITE 66 66 BY SIMILARITY.  
FT DISULFID 73 119 BY SIMILARITY.  
FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).  
SQ SEQUENCE 286 AA; 31211 MW; 82715D986508F50D CRC64;  
Query Match 69.4%; Score 933; DB 1; Length 286;  
Best Local Similarity 67.9%; Pred. No. 7.7e-67;  
Matches 178; Conservative 37; Mismatches 47; Indels 0; Gaps 0;  
QY 2 PETLVKVKDAEDQLGARVGYIELDLNSGEILSEFRSEKRPFMSTFKVLLCGAVLSRIDA 61  
DB 23 PQPLEQIKLSSESQLSGRVGMTEMDLASGRLLTAWRADERFPMSTFKVLLCGAVLARVDA 82  
QY 62 GQEQLGRRIRHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGPK 121  
DB 83 GDEQLERKIHRYQDLDVDSVSEKHLADGMTVGLCAAAITMSDNSANLLLATVGCPA 142  
QY 122 ELTAPFLHNMGDHVRTRLDREWEDELNEALPNDERDITTPVAMATTLRKLLTGLLTLASRQ 181  
DB 143 GLTAFRLRQIGDVTPLDRMETELNEALPGDARDITTPASMAATLRKLLTSQRLSARSQ 202  
QY 182 LIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGRIIALGPDGKPSRIIVITTTGS 241  
DB 203 LLDGMVDDRVAGPLIRSVLPAGWFIADKTGASRGARIGVALLGPNNKAERIVVITLRDT 262  
QY 242 QATMDERNQIAETIGSLIKHW 263  
DB 263 PASMAERNQIAGIGALLIEHW 284  
RESULT 8  
BLAS\_KLEPN STANDARD; PRT; 286 AA.  
AC P37320;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Beta-lactamase SHV-5 precursor (EC 3.5.2.6).  
GN BLA OR SHV5.  
OS Klebsiella pneumoniae, and  
OS Pseudomonas aeruginosa.  
OG Plasmid pPA6-KE.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573, 287;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=K.pneumoniae;  
RX MEDLINE=91207045; PubMed=2088203;  
RA Billoet-Klein D., Gutmann L., Collatz E.;  
RT "Nucleotide sequence of the SHV-5 beta-lactamase gene of a Klebsiella  
RT pneumoniae plasmid."  
RL Antimicrob. Agents Chemother. 34:2439-2441 (1990).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=K.pneumoniae; STRAIN=KPGE-2, and KPPLA-4;  
RX MEDLINE=97291235; PubMed=9145849;  
RA Nuesch-Inderbinen M., Kayser F.H., Hachler H.;  
RT "Survey and molecular genetics of SHV beta-lactamases in  
RT Enterobacteriaceae in Switzerland: two novel enzymes, SHV-11 and  
RT SHV-12."  
RL Antimicrob. Agents Chemother. 41:943-949 (1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=P.aeruginosa;  
RA Scoulica E., Aransay A., Tselentis I.;  
RT "Extended spectrum beta-lactamase SHV-5 in Pseudomonas aeruginosa  
RT clinical strain."  
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS  
CC NOTABLY CEFOTAXIME AND CEFOTAZIDIME. SHV-5 CAUSES PARTICULARLY HIGH  
CC LEVELS OF RESISTANCE TO AZTREONAM AND CEFOTAZIDIME.  
CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
CC amino acid.  
CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.  
CC -----  
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CC -----  
DR EMBL; X55640; CAA39164.1; -.  
DR EMBL; X98103; CAA66731.1; -.  
DR EMBL; X98104; CAA66732.1; -.  
DR EMBL; AF096930; AAC64608.1; -.  
DR PIR; A60632; A60632.  
DR HSSP; P14557; ISHV.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
KW Hydrolase; Antibiotic resistance; Plasmid; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 286 BETA-LACTAMASE SHV-5.  
FT ACT\_SITE 66 66 BY SIMILARITY.  
FT DISULFID 73 119 BY SIMILARITY.  
FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).  
SQ SEQUENCE 286 AA; 31253 MW; 738F426CC51F5FBA CRC64;  
Query Match 69.3%; Score 932; DB 1; Length 286;  
Best Local Similarity 67.6%; Pred. No. 9.2e-67;  
Matches 177; Conservative 39; Mismatches 46; Indels 0; Gaps 0;  
QY 2 PETLVKVKDAEDQLGARVGYIELDLNSGEILSEFRSEKRPFMSTFKVLLCGAVLSRIDA 61  
DB 23 PQPLEQIKLSSESQLSGRVGMTEMDLASGRLLTAWRADERFPMSTFKVLLCGAVLARVDA 82  
QY 62 GQEQLGRRIRHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGPK 121  
DB 83 GDEQLERKIHRYQDLDVDSVSEKHLADGMTVGLCAAAITMSDNSANLLLATVGCPA 142



QY	122 ELTAFLHNNGDHTRLDRMEPELNEALPNDERDTTTPVAMATTLRKLLTGELLTLASRQ	181
	:                 :         :         :	
Dd	143 GLTAFLRQGDNVTRLDRMETELNEALPGDARDTTTPASMAATLRKLLTSQRLSARSGRQ	202
QY	182 LIDWMEADKVAGPLLRSLAPAGWFIADKSGAGERGSRGIHAALGPDGKPSRIWIYTGS	241
	:   :   :       :               :   :       :         :	
Dd	203 LLQWMMVDNRVAGPLIRSVLPAGWFILADKTGASKRGARGIALLGPNNKAERIVILIYLDIT	262
QY	242 QATMDERNRQIAEIGASLIKHW	263
	:   :       :         :       :	
Dd	263 PASMAERNQIAGIGAALIIEHW	284

```

RESULT 9
BLA4_KLEPN
ID      BLA4_KLEPN      STANDARD;      FRT;      265 AA.
AC      P37323;
DT      01-OCT-1994 (Rel. 30, Created)
DT      01-OCT-1994 (Rel. 30, last sequence update)
DT      16-OCT-2001 (Rel. 40, last annotation update)
DE      Beta-lactamase SHV-4 (EC 3.5.2.6) (Ceftazidimase 5) (CAZ-5) .
GN      BLA OR SHV4 .
OS      Klebsiella pneumoniae .
OG      Plasmid pUD21 .
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Klebsiella .
OX      NCBI_TaxID=573;
RN      [1]

```

```

RC STRAIN=210-2;
RX MEDLINE=90146269; PubMed=2694955;
RA Peduzzi J., Barthelemy M., Tiwari K., Mattioli D., Labia R.;
RT "Structural features related to hydrolytic activity against
RT ceftazidime of plasmid-mediated SHV-type CAZ-5 beta-lactamase.";
RL Antimicrob. Agents Chemother. 33:2160-2163(1989).
CC -! FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS
CC NOTABLY CEFOTAXIME AND CEFTAZIDIME. SHV-4 CAUSES PARTICULARLY HIGH
CC LEVELS OF RESISTANCE TO AZTREONAM AND CEFTAZIDIME.
CC -! CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-
CC amino acid.
CC -! SIMILARITY: Belongs to the class-A beta-lactamase family.
CC PIR; A60448; A60448.
DR HSSP; P14557; 1SHV.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolase; Antibiotic resistance; Plasmid.
FT ACT SITE 45 45 BY SIMILARITY.
FT DISULFID 52 98 BY SIMILARITY.
FT BINDING 209 211 SUBSTRATE (BY SIMILARITY).
SQ SEQUENCE 265 AA; 28860 MW; E575CF38B1ADE304 CRC64;

```

Query Match	69.1%;	Score 929;	DB 1;	length 265;
Best Local Similarity	67.6%;	Pred. No. 1.4e-66;		
Matches 177; Conservative	38;	Mismatches 47;	Indels 0;	Gaps 0;

[illegible]

Qy	242	QATMDERNROI	AIEGASL	IHKW	263
		:       :			
Dø	242	PASMAERNQOI	AGI GALL	IHKW	263

RESULT 10	
BLAC KLEPN	
ID _BLAC KLEPN	STANDARD;
	PRT; 279 AA

DT 13-AUG-1987 (Rel. 05, Created)  
DT 13-AUG-1987 (Rel. 05, last sequence update)  
DT 01-OCT-1994 (Rel. 30, last annotation update)  
DE Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).  
OS *Klebsiella pneumoniae*.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; *Klebsiella*.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=LEN-1;  
RX MEDLINE=87030906; PubMed=3533626;  
RA Arakawa Y., Ohta M., Kido N., Fujii Y., Komatsu T., Kato N.;  
RT "Close evolutionary relationship between the chromosomally encoded  
RT beta-lactamase gene of *Klebsiella pneumoniae* and the TEM  
RT beta-lactamase gene mediated by R plasmids.";  
RL FEBS Lett. 207:69-74(1986).  
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
amino acid.

--!- SIMILARITY: Belongs to the class-A beta-lactamase family.

-----

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```

DR EMBL; X04515; CAA28198.1; -.
DR PIR; A24469; A24469.
DR HSSP; P14557; ISHV.
DR InterPro; IPR001466; Beta_lactamase.
DR InterPro; IPR000871; Beta_lactamase_A.
DR Pfam; PF00144; beta-lactamase; 1.
DR PRINTS; PR00118; BLACTAMASEA.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
KW Hydrolase; Antibiotic resistance; Signal.
FT SIGNAL 1 21
FT CHAIN 22 279 BETA-LACTAMASE.
FT ACT_SITE 66 BY SIMILARITY.
FT DISULFID 73 119 BY SIMILARITY.
FT BINDING 230 232 SUBSTRATE (BY SIMILARITY).
SQ SEQUENCE 279 AA; 30269 MW; C5C88E34E6BCDAEB CRC64;

```

Query Match	67.3%	Score 905;	DB 1;	Length 279;
Best Local Similarity	66.7%	Pred. No. 1.2e-64;		
Matches 170;	Conservative 38;	Mismatches 47;	Indels 0;	Gaps 0;

[illegible]

Db 203 LLOQWVDDRVAGPLIRAVLPFGWFIADKTGAGRGARGIVALLGPDGKPERIVYIYLDRT 262  
QY 242 QATMDERNQIAEIG 256  
Db 263 PASMAERNQHTAGIG 277

RESULT 11

BLA6\_KLEPN STANDARD; PRT; 260 AA.  
AC P96348;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Beta-lactamase SHV-6 precursor (EC 3.5.2.6) (Fragment).  
GN BLA OR SHV6.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SLK-47;  
RX MEDLINE=97372563; PubMed=9228783;  
RA Arlet G., Rouveau M., Philippou A.;  
RT "Substitution of alanine for aspartate at position 179 in the SHV-6  
RT extended-spectrum beta-lactamase.";  
RL FEMS Microbiol. Lett. 152:163-167(1997).  
CC -1- FUNCTION: SHV ENZYMES HYDROLYZE BROAD SPECTRUM CEPHALOSPORINS  
CC NOTABLY CEFOTAXIME AND CEFOTAZIDIME.  
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
CC amino acid.  
CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.

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DR EMBL; Y11069; CAA71948.1; -.  
DR HSSP; P14557; ISHV.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
KW Hydrolyase; Antibiotic resistance; Signal.  
FT NON TER 1  
FT SIGNAL 1  
FT CHAIN 12  
FT ACT\_SITE 56  
FT DISULFID 63  
FT BINDING 220  
FT NON TER 260  
SQ SEQUENCE 260 AA; 28157 MW; 26A8E2D43632EAA0 CRC64;

Query Match 65.4%; Score 879; DB 1; Length 260;  
Best Local Similarity 67.7%; Pred. No. 1.3e-62;  
Matches 168; Conservative 35; Mismatches 45; Indels 0; Gaps 0;

QY 2 PETLVKVKDAEDQIGARVGYIELDLNGEILSFSEERFPMSTFKVLLCGAVLSRIDA 61  
Db 13 PQLPEQIKLSQSGLSGRVGMITEMDLASGRITLTAWRADERFPMSTFKVLLCGAVLARVDA 72  
QY 62 GQEQLGRIHYQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSPK 121  
Db 73 GDEQLERKIHRRQDLVDYSPVSEKHLADGNTVRELCSAATMSDNTAANLLTAVGSPA 132  
QY 122 ELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLITGELLTLASRQ 181

Db 133 GLTAFLRQIGDNVTRLDRWETELNEALPGDARATTPASMAATLRKLITSQRLSARSQ 192  
QY 182 LIDWMEADKYAGPLLRSAIPAGWFIADKSGAGRGSRGIIAALGPDGKPSRIVYITTS 241  
Db 193 LLOQWVDDRVAGPLIRSVLPAGWFIADKTGAGRGARGIVALLGPNKKAERIVYIYLDRT 252  
QY 242 QATMDERN 249  
Db 253 PASMAERN 260

RESULT 12

BLA1\_ENTCL STANDARD; PRT; 286 AA.  
AC P18251;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE Beta-lactamase Ohio-1 precursor (EC 3.5.2.6).  
OS Enterobacter cloacae.  
OG Plasmid pDS075.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Enterobacter.  
OX NCBI\_TaxID=550;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91024125; PubMed=2121093;  
RA Shlaes D.M., Currie-McCumber C., Hull A., Behlau I., Kron M.;  
RT "OHIO-1 beta-lactamase is part of the SHV-1 family.";  
RL Antimicrob. Agents Chemother. 34:1570-1576(1990).  
CC -1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
CC amino acid.  
CC -1- SIMILARITY: Belongs to the class-A beta-lactamase family.

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DR EMBL; M33655; AAA72078.1; -.  
DR PIR; A44958; A44958.  
DR HSSP; P14557; ISHV.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
KW Hydrolyase; Antibiotic resistance; Signal; Plasmid.  
FT SIGNAL 1  
FT CHAIN 22  
FT ACT\_SITE 66  
FT DISULFID 73  
FT BINDING 230  
SQ SEQUENCE 286 AA; 31354 MW; 9FE16709361AF9C5 CRC64;

Query Match 65.0%; Score 874; DB 1; Length 286;  
Best Local Similarity 64.5%; Pred. No. 3.6e-62;  
Matches 169; Conservative 39; Mismatches 54; Indels 0; Gaps 0;

QY 2 PETLVKVKDAEDQIGARVGYIELDLNGEILSFSEERFPMSTFKVLLCGAVLSRIDA 61  
Db 23 PQLPEQIKLSQSGLSGSVGMITEMDLARPGTTLTAWRADERFPMSTFKVLLCGAVLARVDA 82  
QY 62 GQEQLGRIHYQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGSPK 121  
Db 83 GDEQLERKIHRRQDLVDYSPVSEKHLADGNTVRELCSAATMSDNTAANLLTAVGSPA 142  
QY 122 ELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLITGELLTLASRQ 181  
Db 143 GLTAFLRQIGDNVTRLDRWETELNEALPGDARATTPASMAATLRKLITSQRLSARSQ 202



Db 106 QSVSISKEMLVITYSPITEKSLSPETVTFGKICQAAVSYSNDNTAANVFDAIGATGNAY 165  
QY 127 LHMNGDHVTRLDMEPELNEAIPNDERDTPVAMATTLRKLLTGELLTLASRQQLDWM 186  
Db 166 MRSIGDEETQDRKEPELNEGTGPDVDRDTPPNAMVNSLRKILLGDALSSRSQQLQWM 225  
QY 187 EADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVVIYTTGSOATMD 246  
Db 226 LDDQVAGALLRASLPSPDWKIADKTGAGGYGSRISIVAVIWPSPKQPLVVGITYTQTKASMQ 285  
QY 247 ERNRQIAEIGASL 259  
Db 286 ASNQAIARIGVVL 298

RESULT 15

BLC3\_PSEAE  
ID BLC3\_PSEAE STANDARD; PRT; 288 AA.  
AC P37322;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Beta-lactamase CARB-3 precursor (EC 3.5.2.6) (Carbenicillinase 3).  
GN CARB3.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=Ci10te; TRANSPOSON=Tn1408;  
RX MEDLINE=91323732; PubMed=1650733;  
RA Lachapelle J., Dufresne J., Levesque R.C.;  
RT "Characterization of the blaCARB-3 gene encoding the  
carbenicillinase-3 beta-lactamase of Pseudomonas aeruginosa.";  
RL Gene 102:7-12(1991).  
CC -!- FUNCTION: HYDROLYZES BOTH CARBENICILLIN AND OXACILLIN.  
CC -!- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-  
CC amino acid.  
CC -!- SIMILARITY: Belongs to the class-A beta-lactamase family.  
CC -----  
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CC -----  
DR EMBL; S46063; AAB19430.2; ALT\_INIT.  
DR PIR; JQ1136; JQ1136.  
DR HSP; P14557; ISHV.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
KW Hydrolase; Antibiotic resistance; Signal; Transposable element.  
FT SIGNAL 1 17 POTENTIAL.  
FT CHAIN 18 288 BETA-LACTAMASE CARB-3.  
FT ACT\_SITE 65 65 BY SIMILARITY.  
FT DISULFID 72 118 BY SIMILARITY.  
FT BINDING 229 231 SUBSTRATE (BY SIMILARITY).  
SQ SEQUENCE 288 AA; 31313 MW; 38EBAF8789201AC6 CRC64;

Query Match 40.1%; Score 539.5; DB 1; Length 288;  
Best Local Similarity 46.0%; Pred. No. 1.2e-35;  
Matches 116; Conservative 42; Mismatches 93; Indels 1; Gaps 1;

QY 8 VKDAEDQLGARVGYTELDINSGEILSFRRSEKPFPMSTFKVLLCGAVLSRIDAGEQLG 67  
Db 29 VKAIEVSLARIGVSVLDLTQNGEYWD-YNGNQRFPLTSTFKTIACAKLLYDAEQGVNPN 87

QY 68 RRIHYSQNDLVEYSPVTEKHLTDGNTVRELCSAATMSDNTAANLLTTIGPKELTAF 127  
Db 88 STVEIKKADLVITYSPVIEKQVGAITLDDACFATMTTSDNTAANIILSAVGGPKGVTD 147  
QY 128 HNMGDHVRDLRMEPELNEAIPNDERDTPVAMATTLRKLLTGELLTLASRQQLDWM 187  
Db 148 RQIGDKETRLDRIEPDLNEGKGLDRLDTPPKAIASTLNKLLFGSALSEMNOQKLESWMV 207  
QY 188 ADKVAGPLLRSLPAGWFIADKSGAGERSGIIAALGPDGKPSRIVVIYTTGSOATMD 247  
Db 208 NNQVTGNLLRSVLPAGWNIADRSAGAGFGARSITAVVWSEHQAPIVISIYLAQTQASMAE 267  
QY 248 RNRQIAEIGASL 259  
Db 268 RNDATVKGHSI 279

Search completed: June 18, 2004, 19:08:28  
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 18:59:13 ; Search time 21 Seconds

(without alignments)  
1204.684 Million cell updates/sec

Title: EPPER526106.PEP  
Perfect score: 1345

Sequence: 1 hpetlvkvkdaedqlgarvy.....tmdermrqiaiegaslikhw 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR 78:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Match length	DB ID	Description
1	1330	98.9	286	2 S47061	beta-lactamase (EC
2	1330	98.9	286	2 T51301	beta-lactamase (EC
3	1330	98.9	286	4 S41975	beta-lactamase (EC
4	1325	98.5	286	1 PNECP	beta-lactamase (EC
5	1325	98.5	286	4 I40905	beta-lactamase (EC
6	1312	97.5	286	2 S60312	extended spectrum
7	1311	97.5	286	2 S30113	beta-lactamase (EC
8	1305	97.0	286	2 S60310	extended spectrum
9	1303	96.9	286	2 S60311	beta-lactamase (EC
10	1299	96.6	286	2 JQ1546	Bla protein - Salm
11	942	70.0	265	2 S00464	beta-lactamase (EC
12	940	69.9	286	2 S16146	beta-lactamase (EC
13	940	69.9	286	2 A60679	beta-lactamase (EC
14	936	69.6	265	2 S02434	beta-lactamase (EC
15	936	69.6	286	1 A44998	beta-lactamase (EC
16	933	69.4	286	2 A37200	beta-lactamase (EC
17	932	69.3	286	2 A60632	beta-lactamase (EC
18	929	69.1	265	2 A60448	beta-lactamase (EC
19	907.5	67.5	287	1 A44996	beta-lactamase (EC
20	897	66.7	279	2 A24469	beta-lactamase (EC
21	874	65.0	286	1 A44958	beta-lactamase (EC
22	672	50.0	298	2 A41381	beta-lactamase (EC
23	539.5	40.1	288	2 JQ1136	beta-lactamase (EC
24	539.5	40.1	304	2 A35001	beta-lactamase (EC
25	535.5	39.8	304	2 A49789	beta-lactamase (EC
26	529.5	39.4	288	2 J50755	beta-lactamase (EC
27	524.5	39.0	281	2 D95395	probable Beta lact
28	524	39.0	105	2 JC2566	bla protein - Pseu
29	521	38.7	276	2 JH0268	beta-lactamase (EC

30	513.5	38.2	291	2 S42075	beta-lactamase (EC
31	512.5	38.1	263	2 A54543	beta-lactamase (EC
32	512.5	38.1	293	2 S04649	beta-lactamase (EC
33	505.5	37.6	302	2 S36188	beta-lactamase (EC
34	496.5	36.9	294	2 S15553	beta-lactamase (EC
35	494.5	36.8	306	1 B45822	beta-lactamase (EC
36	491	36.5	291	2 JF0074	beta-lactamase (EC
37	489.5	36.4	305	2 A60680	beta-lactamase (EC
38	489.5	36.4	305	2 A57002	beta-lactamase (EC
39	489.5	36.4	305	2 A61156	beta-lactamase (EC
40	483.5	35.9	306	2 G69674	beta-lactamase (EC
41	483	35.9	314	2 S06967	beta-lactamase (EC
42	482.5	35.9	306	2 S47330	penicillinase - Ba
43	477	35.5	263	2 S23929	beta-lactamase (EC
44	471.5	35.1	294	2 S19006	beta-lactamase (EC
45	467.5	34.8	309	2 JC4117	beta-lactamase (EC

ALIGNMENTS

RESULT 1  
S47061  
beta-lactamase (EC 3.5.2.6) - phage phi-X174  
C/Species: phage phi-X174  
C/Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 22-Jun-1999  
C/Accession: S47061  
R/Heinrich, B.; Schmidtberger, B.  
submitted to the EMBL Data Library, July 1994  
A/Description: A variant of phiX174 gene E-based positive selection vectors with enhance  
A/Reference number: S47060  
A/Accession: S47061  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-286 <HEN>  
A/Cross-references: EMBL:Z35638; NID:g520996; PIDN:CAA84692.1; PID:g520998  
C/Superfamily: beta-lactamase I  
C/Keywords: hydrolase

Query Match 98.9%; Score 1330; DB 2; Length 286;  
Best Local Similarity 98.9%; Pred. No. 3.5e-103;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	HPETLVKVKDAEDQLGARVGYIELDLNSGELIESFRSEERFPMWSTFKVLLCGAVLSRID	60
DB	24	HPETLVKVKDAEDQLGARVGYIELDLNSGELIESFRPEERFPMWSTFKVLLCGAVLSRID	83
QY	61	AGQEQIGRIHYSQNDLVEYSPYTEKHLTDGWTVRELCSAAITMSDNTAANLLITIGGP	120
DB	84	AGQEQIGRIHYSQNDLVEYSPYTEKHLTDGWTVRELCSAAITMSDNTAANLLITIGGP	143
QY	121	KELTAFILHNMGDHYVTRLDRWEPELNEALPNDERDITTPVAMATTLRKLLTGEILLTASRQ	180
DB	144	KELTAFILHNMGDHYVTRLDRWEPELNEALPNDERDITTPVAMATTLRKLLTGEILLTASRQ	203
QY	181	QLIDWMEADKVAAGPLIRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVITYTG	240
DB	204	QLIDWMEADKVAAGPLIRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIIVITYTG	263
QY	241	SOATMDERNRQIAEIGASLIKHW	263
DB	264	SOATMDERNRQIAEIGASLIKHW	286

RESULT 2  
T51301  
beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe)  
C/Species: Schizosaccharomyces pombe  
C/Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 02-Sep-2000  
C/Accession: T51301  
R/WACH, A.; BRACHAT, A.; ALBERTISEGUI, C.; REBISCHUNG, C.; PHILIPPSEN, P.  
Yeast 13, 1065-1075, 1997  
A/Title: Heterologous His3 marker and GFP reporter modules for PCR-targeting in Saccharo







Db 84 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143  
QY 121 KELTAFIHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFIHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKH 263  
Db 264 SQATMDERNRQIAEIGASLIKH 286

RESULT 5  
I40905  
beta-lactamase (EC 3.5.2.6) - synthetic  
C:Species: synthetic  
A:Note: cloning vector pCG1408 engineered and expressed in *Clavibacter xyli* subsp. *cynod*  
C:Date: 15-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 20-Oct-2000  
C:Accession: I40905  
R:Taylor, J.; Stearman, R.S.; Uratani, B.B.  
Plasmid 29, 241-244, 1993  
A:Title: Development of a native plasmid as a cloning vector in *Clavibacter xyli* subsp.  
A:Reference number: I40904; MUID:93361581; PMID:7689234  
A:Accession: I40905  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-286 <RES>  
A:Cross-references: EMBL:U21228; NID:g885956; PIDN:AAA70411.1; PID:g885958  
C:Keywords: hydrolase

Query Match 98.5%; Score 1325; DB 4; Length 286;  
Best Local Similarity 98.1%; Pred. No. 9.1e-103;  
Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;  
QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMSTFKVLLCGAVLSRD 83  
QY 61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 120  
Db 84 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143  
QY 121 KELTAFIHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFIHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKH 263  
Db 264 SQATMDERNRQIAEIGASLIKH 286

RESULT 6  
S60312  
extended spectrum beta-lactamase CAZ-7 - *Klebsiella pneumoniae*  
C:Species: *Klebsiella pneumoniae*  
C:Date: 12-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 22-Jun-1999  
C:Accession: S60312  
R:Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R.  
Antimicrob. Agents Chemother. 36, 1817-1820, 1992  
A:Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.  
A:Reference number: S60310; MUID:93037315; PMID:1416873  
A:Accession: S60312  
A:Status: preliminary; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-286 <CHA>

A:Cross-references: EMBL:X65254; NID:g296955; PIDN:CAA46346.1; PID:g296956  
C:Superfamily: beta-lactamase I

Query Match 97.5%; Score 1312; DB 2; Length 286;  
Best Local Similarity 97.0%; Pred. No. 1.1e-101;  
Matches 255; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMSTFKVLLCGAVLSRD 83  
QY 61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 120  
Db 84 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143  
QY 121 KELTAFIHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFIHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKH 263  
Db 264 SQATMDERNRQIAEIGASLIKH 286

RESULT 7  
S30113  
beta-lactamase (EC 3.5.2.6) TEM-3 - *Klebsiella pneumoniae* plasmid pCFE04  
C:Species: *Klebsiella pneumoniae*  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 22-Jun-1999  
C:Accession: S30113  
R:Mabilat, C.; Lourencao-Vital, J.; Goussard, S.; Courvalin, P.  
Mol. Gen. Genet. 235, 113-121, 1992  
A:Title: A new example of physical linkage between Tn1 and Tn21: the antibiotic multiple  
A:Reference number: S30112; MUID:93062798; PMID:1331747  
A:Accession: S30113  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-286 <MAB>  
A:Cross-references: EMBL:X64523; NID:g43797; PIDN:CAA45828.1; PID:g43798  
C:Genetics:  
A:Gene: bla(TEM-3)  
A:Genome: plasmid  
C:Superfamily: beta-lactamase I  
C:Keywords: antibiotic resistance; hydrolase

Query Match 97.5%; Score 1311; DB 2; Length 286;  
Best Local Similarity 97.0%; Pred. No. 1.3e-101;  
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Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMSTFKVLLCGAVLSRD 83  
QY 61 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 120  
Db 84 AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGP 143  
QY 121 KELTAFIHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFIHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKH 263  
Db 264 SQATMDERNRQIAEIGASLIKH 286

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RESULT 8
S60310
extended spectrum beta-lactamase CAZ-2 - Klebsiella pneumoniae
C/Species: Klebsiella pneumoniae
C/Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 22-Jun-1999
C/Accession: S60310
R:Chanal, C.; Poupart, M.C.; Sirot, D.; Labia, R.; Sirot, J.; Cluzel, R.
Antimicrob. Agents Chemother. 36, 1817-1820, 1992
A/Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.
A/Reference number: S60310; MUID:93037315; PMID:1416873
A/Accession: S60310
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <CHA>
A/Cross-references: EMBL:X65252; NID:g296951; PIDN:CAA46344.1; PID:g296952
C/Superfamily: beta-lactamase I

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Best Local Similarity	96.6%;	Pred. No. 4.2e-101;		
Matches 254; Conservative	4;	Mismatches 5;	Indels 0;	Gaps 0;

[illegible]

RESULT 9  
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 beta-lactamase (EC 3.5.2.6) TEM-1 - Klebsiella pneumoniae transposon Tn1331  
 C;Species: Klebsiella pneumoniae  
 C;Date: 12-Apr-1996 #sequence revision 19-Apr-1996 #text\_change 22-Jun-1999  
 C;Accession: S60311; F37392; F00498  
 R;Chanal, C.; Poupart, M.C.; Siroit, D.; Labia, R.; Siroit, J.; Cluzel, R.  
 Antimicrob. Agents Chemother. 36, 1817-1820, 1992  
 A;Title: Nucleotide sequences of CAZ-2, CAZ-6, and CAZ-7 beta-lactamase genes.  
 A;Reference number: S60310; MUID:93037315; PMID:1416873  
 A;Accession: S60311  
 A;Status: preliminary; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-286 <CHA>  
 A;Cross-references: EMBL:X65253; NID:g296953; PIDN:CAA46345.1; PID:g296954  
 R;Tolmasky, M.E.  
 Plasmid 24, 218-226, 1990  
 A;Title: Sequencing and expression of aadA, bla, and tnpR from the multiresistance trans-  
 A;Reference number: A37392; MUID:91172904; PMID:1963948  
 A;Accession: F37392  
 A;Molecule type: DNA  
 A;Residues: 1-32 <TOL>  
 A;Cross-references: GB:M55547; NID:g155010; PIDN:AAA98408.1; PID:g155016  
 C;Genetics:  
 A;Gene: TEM-bla  
 C;Superfamily: beta-lactamase I  
 C;Keywords: antibiotic resistance; hydrolase

	Matches	253;	Conservative	5;	Mismatches	5,	Indels	0;	Gaps	0,
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Db	24	HPETLVKVKDAEDQLGARVGYIELDINSGEILLESFRSEERFPMSTMTEKVLICGAVLSRID	:	:	:	:	:	:	:	:
QY	61	AGQEQLGRRIRHYSQNDLVEYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP	:	:	:	:	:	:	:	:
Db	84	AGQEQLGRRIRHYSQNDLVKYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP	:	:	:	:	:	:	:	:
QY	121	KELTAFLHNMGDHYTRLDRLWEPELNEAIPNDERDITTPVAMATTLRKLITGELLTLASRQ	:	:	:	:	:	:	:	:
Db	144	KELTAFLHNMGDHYTRLDRLDWEPELNEAIPNDERDITTPAMATTLRKLITGELLTLASRQ	:	:	:	:	:	:	:	:
QY	181	QLIDWMEADKVAGPLLRISALPAGWFIADKSGAGERGSRGIIALGPDGKPSRIIVITYTG	:	:	:	:	:	:	:	:
Db	204	QLIDWMEADKVAGPLLRISALPAGWFIADKSGTGRGSRGIIALGPDGKPSRIIVITYTG	:	:	:	:	:	:	:	:
QY	241	SQATMDERNRQIAETIGASLLIKHW	:	:	:	:	:	:	:	:
Db	264	SQATMDERNRQIAETIGASLLIKHW	:	:	:	:	:	:	:	:

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RESULT 10
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Bla protein - Salmonella typhimurium plasmid NTP16
N;Alternate names: beta lactamase homolog
C/Species: Salmonella typhimurium
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C/Accession: JQ1546
R;Cannon, P.M.; Strike, P.
Plasmid 27, 220-230, 1992
A;Title: Complete nucleotide sequence and gene organization of plasmid NTP16-
A;Reference number: JQ1538; MUID:92383313; PMID:1325061
A;Accession: JQ1546
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-286 <CAN>
C;Genetics:
A;Genome: Plasmid
C;Superfamily: beta-lactamase I

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DG	24 HEPTLVKVKDAEDDLGDRVGYIELDNSGKILESFRPERFPMMSTFKVLLCGAVLSRVD 83       	:	:	:	:	:
QY	61 AGGEQLGRRIHYSSQNLDVEYSPTVEKHLLTDMGTVRELCSAAITMSDNATAANLIIITIGGP 120       	:	:	:	:	:
DG	84 AGEQLGRRIHISQNDLVEYSPTVEKHLLTDGMTVRELCSAAITMSDNATAANLIIITIGGP 143       	:	:	:	:	:
QY	121 KELTAFLNMGDHVTRLDRWEPELNKAIPNDERDTTPVAMATTLRKLITGELLTIASRQ 180       	:	:	:	:	:
DG	144 KELTSFLNMGDHVTRLDRWEPELNKAIPNDERDTTPAAMATTLRKLLTGELLTIASRQ 203       	:	:	:	:	:
QY	181 QLIDMMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGGDGKPSRIWIYTTG 240       	:	:	:	:	:
DG	204 QLIDMMEADKVAGPLLRSAIPAGWFIAKDSGAGERGYSGLI AALGGDGKPSRIWIYTTG 263       	:	:	:	:	:
QY	241 SQATMDERNRQIAEIGASLIKHW 263       	:	:	:	:	:
DG	264 SQATMDERNRQIAEIGASLIKHW 286       	:	:	:	:	:

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RESULT 11
S00464
beta-lactamase (EC 3.5.2.6) class A - Escherichia coli plasmid p453
N/Alternate names: beta-lactamase PIT-2; beta-lactamase SHV-1
C/Species: Escherichia coli
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1993

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:09:08 ; Search time 49 Seconds  
(without alignments)  
1515.275 Million cell updates/sec

Title: EPPER526106.PEP  
Sequence: 1 hpetlvkvkdaedqlgarvg.....tmdermrqiaiegaslikhw 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1163542 segs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
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8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1330	98.9	263	12	US-10-668-778-2
2	1330	98.9	286	10	US-09-919-901-7
3	1330	98.9	286	10	US-09-919-901-14
4	1330	98.9	286	10	US-09-919-901-21
5	1330	98.9	286	12	US-09-837-306-354
6	1330	98.9	286	14	US-10-191-966-7
7	1330	98.9	286	14	US-10-191-966-14
8	1330	98.9	286	14	US-10-191-966-21
9	1330	98.9	286	15	US-10-045-674-523
10	1330	98.9	2307	10	US-09-919-901-2
11	1330	98.9	2307	10	US-09-919-901-9
12	1330	98.9	2307	10	US-09-919-901-16
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16	1329	98.8	286	14	US-10-231-013-9	Sequence 9, Appli
17	1329	98.8	1293	14	US-10-251-385-292	Sequence 292, App
18	1325	98.5	265	9	US-09-772-114-6	Sequence 6, Appli
19	1325	98.5	265	14	US-10-280-482-2	Sequence 2, Appli
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21	1325	98.5	286	14	US-10-016-668-5	Sequence 5, Appli
22	1325	98.5	286	14	US-10-280-482-4	Sequence 4, Appli
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24	1318	98.0	265	9	US-09-772-114-8	Sequence 8, Appli
25	1318	98.0	265	14	US-10-280-482-6	Sequence 6, Appli
26	1317	97.9	264	9	US-09-772-114-9	Sequence 9, Appli
27	1317	97.9	264	14	US-10-280-482-8	Sequence 8, Appli
28	1310.5	97.4	262	12	US-10-393-449-3	Sequence 3, Appli
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32	539.5	40.1	288	14	US-10-016-668-6	Sequence 6, Appli
33	457	34.0	94	12	US-09-925-298-760	Sequence 760, App
34	457	34.0	94	14	US-10-102-806-760	Sequence 760, App
35	438.5	32.6	321	14	US-10-156-761-11986	Sequence 11986, A
36	433.5	32.2	291	16	US-10-062-188-1	Sequence 1, Appli
37	392	29.1	262	9	US-09-772-114-10	Sequence 10, Appli
38	392	29.1	262	14	US-10-280-482-10	Sequence 10, Appli
39	175	13.0	290	16	US-10-414-532-65	Sequence 65, Appli
40	137	10.2	334	10	US-09-894-159-4	Sequence 4, Appli
41	137	10.2	841	10	US-09-894-159-2	Sequence 2, Appli
42	109	8.1	21	16	US-10-414-532-3	Sequence 3, Appli
43	107.5	8.0	524	16	US-10-414-532-28	Sequence 28, Appli
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45	97	7.2	561	12	US-10-425-114-73015	Sequence 73015, A

ALIGNMENTS

RESULT 1  
US-10-668-778-2  
; Sequence 2, Application US/10668778  
; Publication No. US20040038317A1  
; GENERAL INFORMATION:  
; APPLICANT: Balint, Robert F.  
; APPLICANT: Her, Jeng-Horng  
; APPLICANT: Kalobios, Inc.  
; TITLE OF INVENTION: Interaction-Activated Proteins  
; FILE REFERENCE: 021167-000700US  
; CURRENT APPLICATION NUMBER: US/10/668,778  
; CURRENT FILING DATE: 2003-09-22  
; PRIOR APPLICATION NUMBER: US/09/526,106  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: US 60/124,339  
; PRIOR FILING DATE: 1999-03-15  
; PRIOR APPLICATION NUMBER: US 60/135,926  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: US 60/175,968  
; PRIOR FILING DATE: 2000-01-13  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 263  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
; FEATURE:  
; OTHER INFORMATION: TEM-1 beta-lactamase  
; US-10-668-778-2

Query Match 98.9%; Score 1330; DB 12; Length 263;  
Best Local Similarity 98.9%; Pred. No. 6.5e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db      241 SQATMDERNRQIAETIGASLIKHW 263
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## RESULT 2

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US-09-919-901-7
; Sequence 7, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-7
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Query Match 98.9%; Score 1330; DB 10; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      1 HPETLVKKVKAEDQLGARVGYIELDINSGEILLESFRSEERFPMSTFKVLLCGAVLSRID 60
      |||
Db      24 HPETLVKKVKAEDQLGARVGYIELDINSGEILLESFRSEERFPMSTFKVLLCGAVLSRID 83

QY      61 AGOEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGP 120
      |||
Db      84 AGOEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGP 143

QY      121 KELTAFLNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTIRKLLTGELLTLASRQ 180
      |||
Db      144 KELTAFLNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTIRKLLTGELLTLASRQ 203

QY      181 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 240
      |||
Db      204 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 263

QY      241 SQATMDERNRQIAETIGASLIKHW 263
      |||
Db      264 SQATMDERNRQIAETIGASLIKHW 286
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## RESULT 3

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US-09-919-901-14
; Sequence 14, Application US/09919901
; Publication No. US20030082518A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-14
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Query Match 98.9%; Score 1330; DB 10; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      1 HPETLVKKVKAEDQLGARVGYIELDINSGEILLESFRSEERFPMSTFKVLLCGAVLSRID 60
      |||
Db      24 HPETLVKKVKAEDQLGARVGYIELDINSGEILLESFRSEERFPMSTFKVLLCGAVLSRID 83

QY      61 AGOEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGP 120
      |||
Db      84 AGOEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGP 143

QY      121 KELTAFLNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTIRKLLTGELLTLASRQ 180
      |||
Db      144 KELTAFLNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTIRKLLTGELLTLASRQ 203

QY      181 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 240
      |||
Db      204 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 263

QY      241 SQATMDERNRQIAETIGASLIKHW 263
      |||
Db      264 SQATMDERNRQIAETIGASLIKHW 286
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## RESULT 4

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US-09-919-901-21
; Sequence 21, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
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US-09-919-901-21

Query Match 98.9%; Score 1330; DB 10; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDAEDQLGARVGYIELDLSNGEILSFSEERFPMSTFKVLLCGAVLSRID 60  
DB 24 HPEITLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
DB 84 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KELTAFLEHMGDHTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
DB 144 KELTAFLEHMGDHTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240  
DB 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
DB 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 5

US-09-837-306-354  
; Sequence 354, Application US/09837306  
; Publication No. US20040029113A1  
; GENERAL INFORMATION:  
; APPLICANT: LADNER, ROBERT C.  
; APPLICANT: COHEN, EDWARD H.  
; APPLICANT: NASTRI, HORACIO G.  
; APPLICANT: ROOKEY, KRISTIN L.  
; APPLICANT: HOET, RENE  
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC  
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A  
; FILE REFERENCE: DYAAX/002  
; CURRENT APPLICATION NUMBER: US/09/837,306  
; PRIOR FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/198,069  
; PRIOR FILING DATE: 2000-04-17  
; NUMBER OF SEQ ID NOS: 428  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 354  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: pCESS  
US-09-837-306-354

Query Match 98.9%; Score 1330; DB 12; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDAEDQLGARVGYIELDLSNGEILSFSEERFPMSTFKVLLCGAVLSRID 60  
DB 24 HPEITLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
DB 84 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KELTAFLEHMGDHTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
DB 144 KELTAFLEHMGDHTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240

DB 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263

DB 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 6

US-10-191-966-7  
; Sequence 7, Application US/10191966  
; Publication No. US20030175692A1  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Patick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/10/191,966  
; CURRENT FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US/09/263,933  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/129,611  
; PRIOR FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: :  
US-10-191-966-7

Query Match 98.9%; Score 1330; DB 14; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPEITLVKVKDAEDQLGARVGYIELDLSNGEILSFSEERFPMSTFKVLLCGAVLSRID 60  
DB 24 HPEITLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
DB 84 AGQEQLGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KELTAFLEHMGDHTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
DB 144 KELTAFLEHMGDHTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 240  
DB 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
DB 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 7

US-10-191-966-14  
; Sequence 14, Application US/10191966  
; Publication No. US20030175692A1  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Patick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/10/191,966  
; CURRENT FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US/09/263,933



;; PRIOR FILING DATE: 1999-03-08  
;; PRIOR APPLICATION NUMBER: 09/129,611  
;; PRIOR FILING DATE: 1998-08-05  
;; NUMBER OF SEQ ID NOS: 33  
;; SOFTWARE: Patentln Ver. 2.0  
;; SEQ ID NO 14  
;; LENGTH: 286  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: :  
US-10-191-966-14

Query Match 98.9%; Score 1330; DB 14; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 60  
|||  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
|||  
Db 84 AGQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KELTAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
|||  
Db 144 KELTAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 240  
|||  
Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
|||  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 8  
US-10-191-966-21  
; Sequence 21, Application US/10191966  
; Publication No. US20030175692A1  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Patick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/10/191,966  
; CURRENT FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US/09/263,933  
; PRIOR FILING DATE: 1999-03-08  
; PRIOR APPLICATION NUMBER: 09/129,611  
; PRIOR FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: :  
US-10-191-966-21

Query Match 98.9%; Score 1330; DB 14; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 60  
|||  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
|||  
Db 84 AGQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KELTAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
|||  
Db 144 KELTAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 240  
|||  
Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
|||  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 9  
US-10-045-674-523  
; Sequence 523, Application US/10045674  
; Publication No. US2003023233A1  
; GENERAL INFORMATION:  
; APPLICANT: LADNER, ROBERT C.  
; APPLICANT: COHEN, EDWARD H.  
; APPLICANT: NASTRI, HORACIO G.  
; APPLICANT: ROOKEY, KRISTIN L.  
; APPLICANT: HOET, RENE  
; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.  
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING  
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY  
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL  
; TITLE OF INVENTION: LIBRARIES  
; FILE REFERENCE: DYAX/002 CIP2  
; CURRENT APPLICATION NUMBER: US/10/045,674  
; CURRENT FILING DATE: 2001-10-25  
; PRIOR APPLICATION NUMBER: 60/198,069  
; PRIOR FILING DATE: 2000-04-17  
; PRIOR APPLICATION NUMBER: 09/837,306  
; PRIOR FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 635  
; SOFTWARE: Patentln Ver. 2.1  
; SEQ ID NO 523  
; LENGTH: 286  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS  
US-10-045-674-523

Query Match 98.9%; Score 1330; DB 15; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.3e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 60  
|||  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
|||  
Db 84 AGQEQGLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KELTAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
|||  
Db 144 KELTAFLLHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 240  
|||  
Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
|||  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

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RESULT 10
US-09-919-901-2
; Sequence 2, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-2
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Query Match 98.9%; Score 1330; DB 10; Length 2307;  
Best Local Similarity 98.9%; Pred. No. 1.5e-127;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGILESFRSEERFPMMSTFKVLLCGAVLSRID 60
Db 2045 HPETLVKVKDAEDQLGARVGYIELDLNSGILESFRSEERFPMMSTFKVLLCGAVLSRID 2104
QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMYVRELCSAAITMSDNTAANLLTTIGSP 120
Db 2105 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMYVRELCSAAITMSDNTAANLLTTIGSP 2164
QY 121 KELTAFLLNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KELTAFLLNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKSRIVITYTGG 240
Db 2225 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKSRIVITYTGG 2284
QY 241 SQATMDERNRQIAEIGASLIKHW 263
Db 2285 SQATMDERNRQIAEIGASLIKHW 2307
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RESULT 11
US-09-919-901-9
; Sequence 9, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
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; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-9
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Query Match 98.9%; Score 1330; DB 10; Length 2307;  
Best Local Similarity 98.9%; Pred. No. 1.5e-127;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGILESFRSEERFPMMSTFKVLLCGAVLSRID 60
Db 2045 HPETLVKVKDAEDQLGARVGYIELDLNSGILESFRSEERFPMMSTFKVLLCGAVLSRID 2104
QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMYVRELCSAAITMSDNTAANLLTTIGSP 120
Db 2105 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMYVRELCSAAITMSDNTAANLLTTIGSP 2164
QY 121 KELTAFLLNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180
Db 2165 KELTAFLLNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 2224
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKSRIVITYTGG 240
Db 2225 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKSRIVITYTGG 2284
QY 241 SQATMDERNRQIAEIGASLIKHW 263
Db 2285 SQATMDERNRQIAEIGASLIKHW 2307
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RESULT 12
US-09-919-901-16
; Sequence 16, Application US/09919901
; Publication No. US20030082518A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-16
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Query Match 98.9%; Score 1330; DB 10; Length 2307;  
Best Local Similarity 98.9%; Pred. No. 1.5e-127;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 2045 HPETLVKVKDAEDQLGARVGYIELDLNSGILESFRSEERFPMMSTFKVLLCGAVLSRID 2104
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Db 2105 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMYVRELCSAAITMSDNTAANLLTTIGSP 2164
QY 121 KELTAFLLNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180
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DB 2165 KELLTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTIRKLLTGELLTLASRQ 2224
QY 181 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIVITYTTG 240
DB 2225 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIVITYTTG 2284
QY 241 SQATMDERNRQIAEIGASLIKHW 263
DB 2285 SQATMDERNRQIAEIGASLIKHW 2307

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## RESULT 13

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US-10-191-966-2
; Sequence 2, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ. ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-2

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Query Match          98.9%; Score 1330; DB 14; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.5e-127;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILSFRRSEERFPMSTFKVLLCGAVLSRID 60
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DB 2105 AGQEQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGP 2164
QY 121 KELTAFILHNMGDHTVTRLDRWEPELNEAIPNDERDTTTPVAMATTIRKLLTGELLTLASRQ 180
DB 2165 KELTAFILHNMGDHTVTRLDRWEPELNEAIPNDERDTTTPVAMATTIRKLLTGELLTLASRQ 2224
QY 181 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIVITYTTG 240
DB 2225 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIVITYTTG 2284
QY 241 SQATMDERNRQIAEIGASLIKHW 263
DB 2285 SQATMDERNRQIAEIGASLIKHW 2307

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## RESULT 14

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US-10-191-966-9
; Sequence 9, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT

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; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-9

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Query Match          98.9%; Score 1330; DB 14; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.5e-127;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 61 AGQEQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGP 120
DB 2105 AGQEQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGP 2164
QY 121 KELTAFILHNMGDHTVTRLDRWEPELNEAIPNDERDTTTPVAMATTIRKLLTGELLTLASRQ 180
DB 2165 KELTAFILHNMGDHTVTRLDRWEPELNEAIPNDERDTTTPVAMATTIRKLLTGELLTLASRQ 2224
QY 181 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIVITYTTG 240
DB 2225 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGAGERSRGIITIALGPDGKPSRIVITYTTG 2284
QY 241 SQATMDERNRQIAEIGASLIKHW 263
DB 2285 SQATMDERNRQIAEIGASLIKHW 2307

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## RESULT 15

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US-10-191-966-16
; Sequence 16, Application US/10191966
; Publication No. US20030175692A1
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/10/191,966
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US/09/263,933
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 2307
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-10-191-966-16

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Query Match          98.9%; Score 1330; DB 14; Length 2307;
Best Local Similarity 98.9%; Pred. No. 1.5e-127;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY	61	AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTGGP	120
Db	2105	AGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTGGP	2164
QY	121	KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDPTTPVAMATTLRKLLTGELLTLASRQ	180
Db	2165	KELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDPTTPVAMATTLRKLLTGELLTLASRQ	2224
QY	181	QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVITYTG	240
Db	2225	QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVITYTG	2284
QY	241	SQATMDERNRQIAETGASLIKHW	263
Db	2285	SQATMDERNRQIAETGASLIKHW	2307

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Job time : 51 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:06:58 ; Search time 22 Seconds

(without alignments)  
617.165 Million cell updates/sec

Title: EPPER526106.PEP  
Perfect score: 1345

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Gapop 10.0 , Gapext 0.5

Searched: 389414 segs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
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2	1330	98.9	286	1 US-08-339-658-2	Sequence 2, Appli
3	1330	98.9	286	3 US-09-263-933-7	Sequence 7, Appli
4	1330	98.9	286	3 US-09-263-933-14	Sequence 14, Appli
5	1330	98.9	286	3 US-09-263-933-21	Sequence 21, Appli
6	1330	98.9	286	4 US-09-025-769B-265	Sequence 265, App
7	1330	98.9	286	4 US-09-025-769B-362	Sequence 362, App
8	1330	98.9	286	4 US-09-919-901-7	Sequence 7, Appli
9	1330	98.9	286	4 US-09-919-901-14	Sequence 14, Appli
10	1330	98.9	286	4 US-09-919-901-21	Sequence 21, Appli
11	1330	98.9	299	4 US-09-025-769B-285	Sequence 285, App
12	1330	98.9	299	4 US-09-025-769B-298	Sequence 298, App
13	1330	98.9	299	4 US-09-025-769B-300	Sequence 300, App
14	1330	98.9	2307	3 US-09-263-933-2	Sequence 2, Appli
15	1330	98.9	2307	3 US-09-263-933-9	Sequence 9, Appli
16	1330	98.9	2307	3 US-09-263-933-16	Sequence 16, Appli
17	1330	98.9	2307	4 US-09-919-901-2	Sequence 2, Appli
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19	1330	98.9	2307	4 US-09-919-901-16	Sequence 16, Appli
20	1329	98.8	286	4 US-09-555-510B-9	Sequence 9, Appli
21	1329	98.8	1293	4 US-09-170-496D-292	Sequence 292, App
22	1329	98.8	1293	4 US-09-364-425B-57	Sequence 57, Appli
23	1325	98.5	263	1 US-08-407-544-2	Sequence 2, Appli
24	1325	98.5	265	2 US-08-719-697-2	Sequence 2, Appli
25	1325	98.5	265	3 US-08-727-616A-2	Sequence 2, Appli
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28	1325	98.5	286	3 US-08-727-616A-4	Sequence 4, Appli
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32	1318	98.0	265	3 US-08-727-616A-6	Sequence 6, Appli
33	1318	98.0	265	4 US-09-481-756-6	Sequence 6, Appli
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35	1317	97.9	264	3 US-08-727-616A-8	Sequence 8, Appli
36	1317	97.9	264	4 US-09-481-756-8	Sequence 8, Appli
37	1310.5	97.4	262	4 US-09-626-581D-3	Sequence 3, Appli
38	1310.5	97.4	262	4 US-09-415-765B-3	Sequence 3, Appli
39	1310.5	97.4	262	4 US-09-626-580C-3	Sequence 3, Appli
40	1308	97.2	286	1 US-08-346-333-16	Sequence 16, Appli
41	1308	97.2	286	5 PCT-US91-07506-16	Sequence 16, Appli
42	942	70.0	313	4 US-09-489-039A-11425	Sequence 11425, A
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ALIGNMENTS

RESULT 1  
US-07-721-775A-2  
; Sequence 2, Application US/07721775A  
; Patent No. 5180666  
; GENERAL INFORMATION:  
; APPLICANT: States, J. Christopher  
; APPLICANT: Hines, Ronald N.  
; APPLICANT: No. 5180666ak, Raymond F.  
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING  
; NUMBER OF INVENTIONS: 2  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Reising, Echington, Barnard, Perry & Milton  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: U.S.A.  
; ZIP: 48099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/721, 775A  
; FILING DATE: 19910627  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I.  
; REGISTRATION NUMBER: 30,955  
; REFERENCE/DOCKET NUMBER: P-321WSU  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (313) 689-3554  
; TELEFAX: (313) 689-4071  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 286 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-07-721-775A-2

Query Match 98.9%; Score 1330; DB 1; Length 286;  
Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 HPETLVKVKDAEDQLGARVGYIELDLNGSKILESFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLNGSKILESFRSEERFPMMSTFKVLLCGAVLSRID 83

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QY 61 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120
Db 84 AGGQQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143
QY 121 KELLTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180
Db 144 KELLTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVITYTTG 240
Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVITYTTG 263
QY 241 SQATMDERNRQIAEIGASLIKHW 263
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 2
US-08-339-658-2
; Sequence 2, Application US/08339658
; Patent No. 5525482
; GENERAL INFORMATION:
; APPLICANT: States, J. Christopher
; APPLICANT: Hines, Ronald N.
; APPLICANT: NO. 5525482ak, Raymond F.
; TITLE OF INVENTION: METHOD AND CELL LINE FOR TESTING
; TITLE OF INVENTION: MUTAGENICITY OF A CHEMICAL
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: U.S.A.
; ZIP: 48099
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/339,658
; FILING DATE: 15-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/990,295
; FILING DATE: 09-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-321WSU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (313) 689-3554
; TELEFAX: (313) 689-4071
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-339-658-2

Query Match 98.9%; Score 1330; DB 1; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.1e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVITYTTG 240
Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVITYTTG 263
QY 241 SQATMDERNRQIAEIGASLIKHW 263
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 3
US-09-263-933-7
; Sequence 7, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; US-09-263-933-7

Query Match 98.9%; Score 1330; DB 3; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.1e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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RESULT 4
US-09-263-933-14
; Sequence 14, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
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; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-14

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Query Match	98.9%;	Score 1330;	DB 3;	Length 286;
Best Local Similarity	98.9%;	Pred. No. 7.1e-139;		
Matches 260;	Conservative	1;	Mismatches 2;	Indels 0;
				Gaps 0;

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QY	121	KELTAFHNMGDHTRLDRWEPEINEAI PNDERDITTPVAMATTLKLLTGELLTLASRQ	180
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QY	181 QLIDMNEADKVAGPLLRSAIPAGFIADKSGAGERGSRGIIAALGPDKPSRIIVVIYTTG 240
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RESULT 5
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; Sequence 21, Application US/09263933
; Patent No. 6280940
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/263,933
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: 09/129,611
; EARLIER FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
US-09-263-933-21

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Query Match	98.9%;	Score 1330;	DB 3;	Length 286;
Best Local Similarity	98.9%;	Pred. No. 7.1e-139;		
Matches 260;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;

QY	1 HPEITLVKVDADQLGARVGIETDLSNGEILSFRRSEERFPMSTFKVLICGAVLSRID	60
DQ	24 HPEITLVKVDADQLGARVGIETDLSNGEILSFRRSEERFPMSTFKVLICGAVLSRID	83

QY	61	AGOEOLGRIHYSONDLVEESPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP	120
D0	84	AGOEOLGRIHYSONDLVEESPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTTGGP	143

QY 121 KELTSALHMGDHTRLDRWEPELNEAI PNDERDTTTPVAMATTLRKL TGELLTLASRQ 180

Db 144 KETLAFILHMGDHTRLDRMEBELNEAIPNDERDITPMYAMATTLRKLLTGELLTIASRQ 203

Qy	181	QI	D	N	E	A	D	K	V	A	G	P	L	L	R	S	A	L	P	A	G	M	F	I	A	D	K	S	G	A	G	E	R	G	I	A	L	G	P	D	G	K	P	S	R	I	V	I	Y	T	T	G	240	
Db	204	Q	I	D	N	E	A	D	K	V	A	G	P	L	L	R	S	A	L	P	A	G	M	F	I	A	D	K	S	G	A	G	E	R	G	I	A	L	G	P	D	G	K	P	S	R	I	V	I	Y	T	T	G	263

Qy	241	SOATMDERNRQIAEIGASLKH	263
Db	264	SOATMDERNRQIAEIGASLKH	286

RESULT 6  
US-09-025-769B-265  
; Sequence 265, Application US/09025769B

```

: GENERAL INFORMATION:
: APPLICANT: Knappik, Achim
: APPLICANT: Pack, Peter
: APPLICANT: Ilag, Vic
: APPLICANT: Ge, Liming
: APPLICANT: Moroney, Simon
: APPLICANT: Plueckthun, Andreas
: TITLE OF INVENTION: Protein/(Poly)peptide libraries
: NUMBER OF SEQUENCES: 373
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10021
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/025,769B
: FILING DATE: 18-FEB-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: EP 95 11 3021.0
: FILING DATE: 18-AUG-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: James F. Haley, Jr., Esq.
: REGISTRATION NUMBER: 27,794
: REFERENCE/DOCKET NUMBER: MORPHO/5
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)596-9000
: TELEFAX: (212)596-9090
: INFORMATION FOR SEQ ID NO: 265:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 286 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: OS-09-025-769B-265

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Query Match	98.9%	Score 1330	DB 4	Length 286
Best Local Similarity	98.9%	Pred. No. 7.1e-139		
Matches 260	Conservative 1	Mismatches 2	Indels 0	Gaps 0

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OY      1 HPETLVKVDADQLGARVGYIELDNLSGEITLESFRSEERFPMSTFKLLCGAVSRID 60
        |||||
DB      24 HPEITLVKVDADQLGARVGVIYELDLNSGKITLESFRPEERFPMSTFKLLCGAVSRID 83
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Qy	Db
61 AGCQGLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGP	120
84 AGCQGLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGP	143

QY	121	KELTAFLHMGDHTRLDRWEPELNEAIPNDERDPTTPVAMATTLRLKLTGELLTLASRQ	180
DB	144	KELTAFLHMGDHTRLDRWEPELNEAIPNDERDPTTPVAMATTLRLKLTGELLTLASRQ	203

QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVITYTTG 240  
 Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVITYTTG 263  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 7

US-09-025-769B-362  
 ; Sequence 362, Application US/09025769B  
 ; Patent No. 6300064  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Knappik, Achim  
 ; APPLICANT: Pack, Peter  
 ; APPLICANT: Ilag, Vic  
 ; APPLICANT: Ge, Jiming  
 ; APPLICANT: Moroney, Simon  
 ; APPLICANT: Plueckhuhn, Andreas  
 ; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 ; NUMBER OF SEQUENCES: 373  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10021  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/025,769B  
 ; FILING DATE: 18-FEB-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 95 11 3021.0  
 ; FILING DATE: 18-AUG-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: James F. Haley, Jr., Esq.  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: MORPHO/5  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212)596-9000  
 ; TELEFAX: (212)596-9090  
 ; INFORMATION FOR SEQ ID NO: 362:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 286 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-025-769B-362

Query Match 98.9%; Score 1330; DB 4; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 60  
 Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMWSTFKVLLCGAVLSRID 83  
 QY 61 AGQEQGLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
 Db 84 AGQEQGLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143  
 QY 121 KELTAFILHNMGDHYTRLDKRWEPNELNEAIPNDRDITTPVAMATTLRKLLTGLLTLASRQ 180  
 Db 144 KELTAFILHNMGDHYTRLDKRWEPNELNEAIPNDRDITTPVAMATTLRKLLTGLLTLASRQ 203  
 QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVITYTTG 240

Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVITYTTG 263  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 8

US-09-919-901-7  
 ; Sequence 7, Application US/09919901  
 ; Patent No. 6599738  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Potts, Karen E.  
 ; APPLICANT: Jackson, Roberta L.  
 ; APPLICANT: Patrick, Amy K.  
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
 ; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
 ; FILE REFERENCE: 0125-0005A  
 ; CURRENT APPLICATION NUMBER: US/09/919,901  
 ; PRIOR FILING DATE: 2001-08-02  
 ; PRIOR APPLICATION NUMBER: 09/263,933  
 ; PRIOR FILING DATE: 1999-02-08  
 ; PRIOR APPLICATION NUMBER: 09/129,611  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentin Ver. 2.0  
 ; SEQ ID NO 7  
 ; LENGTH: 286  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: :  
 ; US-09-919-901-7

Query Match 98.9%; Score 1330; DB 4; Length 286;  
 Best Local Similarity 98.9%; Pred. No. 7.1e-139;  
 Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 60  
 Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMWSTFKVLLCGAVLSRID 83  
 QY 61 AGQEQGLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
 Db 84 AGQEQGLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143  
 QY 121 KELTAFILHNMGDHYTRLDKRWEPNELNEAIPNDRDITTPVAMATTLRKLLTGLLTLASRQ 180  
 Db 144 KELTAFILHNMGDHYTRLDKRWEPNELNEAIPNDRDITTPVAMATTLRKLLTGLLTLASRQ 203  
 QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVITYTTG 240  
 Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVITYTTG 263  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 9

US-09-919-901-14  
 ; Sequence 14, Application US/09919901  
 ; Patent No. 6599738  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Potts, Karen E.  
 ; APPLICANT: Jackson, Roberta L.  
 ; APPLICANT: Patrick, Amy K.  
 ; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
 ; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
 ; FILE REFERENCE: 0125-0005A  
 ; CURRENT APPLICATION NUMBER: US/09/919,901  
 ; CURRENT FILING DATE: 2001-08-02

; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 14
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-14

Query Match 98.9%; Score 1330; DB 4; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.1e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSSEKPPMSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGGP 120
DB 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGGP 143
QY 121 KELTAPFLHNMGDHVTTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAPFLHNMGDHVTTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYTG 263
QY 241 SQATMDERNRQIAEIGASLIKHW 263
DB 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 10
US-09-919-901-21
; Sequence 21, Application US/09919901
; Patent No. 6599738
; GENERAL INFORMATION:
; APPLICANT: Potts, Karen E.
; APPLICANT: Jackson, Roberta L.
; APPLICANT: Patrick, Amy K.
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE
; FILE REFERENCE: 0125-0005A
; CURRENT APPLICATION NUMBER: US/09/919,901
; CURRENT FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 09/263,933
; PRIOR FILING DATE: 1999-02-08
; PRIOR APPLICATION NUMBER: 09/129,611
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 21
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION:
US-09-919-901-21

Query Match 98.9%; Score 1330; DB 4; Length 286;
Best Local Similarity 98.9%; Pred. No. 7.1e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSSEKPPMSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGGP 120
DB 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGGP 143
QY 121 KELTAPFLHNMGDHVTTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180
DB 144 KELTAPFLHNMGDHVTTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYTG 240
DB 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYTG 263
QY 241 SQATMDERNRQIAEIGASLIKHW 263
DB 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 11
US-09-025-769B-285
; Sequence 285, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilaq, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 285:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-285

Query Match 98.9%; Score 1330; DB 4; Length 299;
Best Local Similarity 98.9%; Pred. No. 7.6e-139;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSSEKPPMSTFKVLLCGAVLSRID 60
DB 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRID 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANILLTTIGGP 120

Db 84 AGQEQLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143  
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QOLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 240  
Db 204 QOLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 12

US-09-025-769B-298  
; Sequence 298, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 298:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 299 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-298

Query Match 98.9%; Score 1330; DB 4; Length 299;  
Best Local Similarity 98.9%; Pred. No. 7.6e-139;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRSEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120  
Db 84 AGQEQLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143

QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QOLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 240  
Db 204 QOLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 13

US-09-025-769B-300  
; Sequence 300, Application US/09025769B  
; Patent No. 6300064  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; APPLICANT: Pack, Peter  
; APPLICANT: Ilag, Vic  
; APPLICANT: Ge, Liming  
; APPLICANT: Moroney, Simon  
; APPLICANT: Plueckhuhn, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769B  
; FILING DATE: 18-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 300:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 299 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-025-769B-300

Query Match 98.9%; Score 1330; DB 4; Length 299;  
Best Local Similarity 98.9%; Pred. No. 7.6e-139;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSEERFPMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRSEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120  
Db 84 AGQEQLGRRIHYSQNDLVEYSPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143  
QY 121 KELTAFILNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180

Db 144 KETLAFHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 14

US-09-263-933-2  
; Sequence 2, Application US/09263933  
; Patent No. 6280940  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Patrick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/09/263,933  
; CURRENT FILING DATE: 1999-03-08  
; EARLIER APPLICATION NUMBER: 09/129,611  
; EARLIER FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 2307  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
US-09-263-933-2

Query Match 98.9%; Score 1330; DB 3; Length 2307;  
Best Local Similarity 98.9%; Pred. No. 1.8e-137;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 60  
Db 2045 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 2104  
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 2105 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 2164  
QY 121 KETLAFHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 180  
Db 2165 KETLAFHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 2224  
QY 181 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 240  
Db 2225 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 2284  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 2285 SQATMDERNRQIAEIGASLIKHW 2307

RESULT 15

US-09-263-933-9  
; Sequence 9, Application US/09263933  
; Patent No. 6280940  
; GENERAL INFORMATION:  
; APPLICANT: Potts, Karen E.  
; APPLICANT: Jackson, Roberta L.  
; APPLICANT: Patrick, Amy K.  
; TITLE OF INVENTION: REPORTER GENE SYSTEM FOR USE IN CELL-BASED ASSESSMENT  
; TITLE OF INVENTION: OF INHIBITORS OF THE HEPATITIS C VIRUS PROTEASE  
; FILE REFERENCE: 0125-0005A  
; CURRENT APPLICATION NUMBER: US/09/263,933  
; CURRENT FILING DATE: 1999-03-08

; EARLIER APPLICATION NUMBER: 09/129,611  
; EARLIER FILING DATE: 1998-08-05  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 2307  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
US-09-263-933-9

Query Match 98.9%; Score 1330; DB 3; Length 2307;  
Best Local Similarity 98.9%; Pred. No. 1.8e-137;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 60  
Db 2045 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 2104  
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 2105 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 2164  
QY 121 KETLAFHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 180  
Db 2165 KETLAFHNMGDHVTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 2224  
QY 181 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 240  
Db 2225 QLIDWMEADKVAAGPLRLSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVVIYTTG 2284  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 2285 SQATMDERNRQIAEIGASLIKHW 2307

Search completed: June 18, 2004, 19:10:35  
Job time : 23 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 19:01:08 ; Search time 45 Seconds

(without alignments)  
1844.029 Million cell updates/sec

Title: EPPER526106.PEP  
Perfect score: 1345  
Sequence: 1 hpetlvkvkdaedqlgarvg.....tmdermrqiaiegaslikhw 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1330	98.9	286	2	Q00626	Q00626 staphylococ
2	1330	98.9	286	9	Q38058	Q38058 bacterioph
3	1327	98.7	286	2	Q8KQ72	Q8KQ72 escherichia
4	1325	98.5	286	2	Q9R748	Q9R748 klebsiella
5	1322	98.3	286	2	Q8KSD2	Q8KSD2 escherichia
6	1322	98.3	286	2	Q34176	Q34176 klebsiella
7	1321	98.2	286	2	Q9LAC0	Q9LAC0 proteus mir
8	1321	98.2	286	2	Q93A80	Q93A80 escherichia
9	1321	98.2	286	2	Q9AGJ5	Q9AGJ5 escherichia
10	1321	98.2	286	2	Q9R435	Q9R435 klebsiella
11	1321	98.2	286	2	Q9RMS2	Q9RMS2 escherichia
12	1321	98.2	286	2	Q8KMX4	Q8KMX4 escherichia
13	1321	98.2	286	2	Q8KSD3	Q8KSD3 klebsiella
14	1321	98.2	286	2	Q9RN48	Q9RN48 escherichia
15	1321	98.2	286	2	Q32372	Q32372 capnocytoph
16	1321	98.2	286	2	Q932Y6	Q932Y6 pseudomonas

17	1320	98.1	286	2	Q9R745	Q9R745 escherichia
18	1320	98.1	286	2	Q8KRH0	Q8KRH0 klebsiella
19	1320	98.1	286	2	Q93A77	Q93A77 escherichia
20	1319	98.1	286	2	Q9S678	Q9S678 klebsiella
21	1319	98.1	286	2	Q9FAA2	Q9FAA2 escherichia
22	1319	98.1	286	2	Q8VP43	Q8VP43 klebsiella
23	1319	98.1	286	2	Q48406	Q48406 klebsiella
24	1319	98.1	286	2	Q8GA85	Q8GA85 escherichia
25	1319	98.1	286	2	Q844X1	Q844X1 klebsiella
26	1318	98.0	286	2	Q9AF08	Q9AF08 escherichia
27	1318	98.0	286	2	Q9S679	Q9S679 escherichia
28	1318	98.0	286	2	Q8L1Y1	Q8L1Y1 escherichia
29	1318	98.0	286	2	P78144	P78144 escherichia
30	1318	98.0	286	2	Q9RMS4	Q9RMS4 escherichia
31	1318	98.0	286	2	Q91UY8	Q91UY8 pseudomonas
32	1318	98.0	286	2	Q9EYX1	Q9EYX1 escherichia
33	1317	97.9	263	2	Q9R2G5	Q9R2G5 escherichia
34	1317	97.9	286	2	Q93A79	Q93A79 escherichia
35	1317	97.9	286	2	Q9R429	Q9R429 morganelia
36	1317	97.9	286	2	Q937J3	Q937J3 escherichia
37	1316	97.8	286	2	Q8RQ59	Q8RQ59 klebsiella
38	1316	97.8	286	2	Q8RPY9	Q8RPY9 enterobacte
39	1316	97.8	286	2	Q9R312	Q9R312 proteus mir
40	1316	97.8	286	2	Q46954	Q46954 escherichia
41	1315	97.8	286	2	Q93G13	Q93G13 klebsiella
42	1315	97.8	286	2	Q8KMX3	Q8KMX3 escherichia
43	1315	97.8	286	2	Q9ZFV9	Q9ZFV9 morganelia
44	1314	97.7	286	2	Q933Z8	Q933Z8 escherichia
45	1314	97.7	286	2	Q9AEY6	Q9AEY6 klebsiella

ALIGNMENTS

RESULT 1  
Q00626 PRELIMINARY; PRT; 286 AA.  
AC Q00626; Q57339; Q08022; Q08102; Q09490; Q09483; Q09393; Q09396;  
AC Q09397; Q09398; Q09399; Q09400; Q09401; Q09402; Q09403; Q09404;  
AC Q09405; Q09406; Q09407; Q09408; Q09481; Q09482;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)  
DE Beta-lactamase precursor (EC 3.5.2.6) (Penicillinase).  
GN BLA OR AMPR.  
GN Staphylococcus aureus,  
OS Escherichia coli,  
OS unidentified, and  
OS Alcaligenes hydrogophilus.  
OG Plasmid pUD84, plasmid pRP4 and plasmid pRAY-1.  
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.  
OX NCBI\_TaxID=1280, 562, 32644, 516;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lieberman B.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Needham C., Noble W.C., Dyke K.G.H.;  
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Maneewannakul K., Maneewannakul S., Ippen-Thler K.;  
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RA Kovach M.E.;  
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RA STRAIN=KT1;  
RC MEDLINE=97074643; PubMed=8917070;  
RX Serebrijski I.G., Vassin V.M., Tsygankov Y.D.;



RT "Two new members of the bio B superfamily: cloning, sequencing and  
RT expression of bio B genes of Methylobacillus flagellatum and  
RT Corynebacterium glutamicum.";  
RL Gene 175:15-22(1996).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RA Rondot S., Anthony K., Dubel S., Ida N., Beyreuther K., Frost L.,  
RA Little M., Breittling F.;  
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96366236; PubMed=8770413;  
RA Rees S., Coote J., Stables J., Goodson S., Harris S., Lee M.G.;  
RT "Bicistronic vector for the creation of stable mammalian cell lines  
RT that predisposes all antibiotic-resistant cells to express recombinant  
RT protein.";  
RL Biotechniques 20:102-104(1996).  
RN [8]  
RP SEQUENCE FROM N.A.  
RA Lou Y., Holtz A.;  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
RN [9]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97105907; PubMed=8948655;  
RA Storck T., Krueh U., Kolhekar R., Sprengel R., Seeburg P.H.;  
RT "Rapid construction in yeast of complex targeting vectors for gene  
RT manipulation in the mouse.";  
RL Nucleic Acids Res. 24:4594-4596(1996).  
RN [10]  
RP SEQUENCE FROM N.A.  
RA Lu Q.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A.  
RA Holtz A., Lou Y.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92302280; PubMed=1319065;  
RA Gossen M., Bujard H.;  
RT "Tight control of gene expression in mammalian cells by tetracycline-  
RT responsive promoters.";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:5547-5551(1992).  
RN [13]  
RP SEQUENCE FROM N.A.  
RA Gossen M., Bujard H.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [14]  
RP SEQUENCE FROM N.A.  
RA Holtz A., Lou Y.;  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
RN [15]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96032859; PubMed=7567477;  
RA Baron U., Freundlieb S., Gossen M., Bujard H.;  
RT "Co-regulation of two gene activities by tetracycline via a  
RT bidirectional promoter.";  
RL Nucleic Acids Res. 23:3605-3606(1995).  
RN [16]  
RP SEQUENCE FROM N.A.  
RA Baron U., Freundlieb S., Gossen M., Bujard H.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [17]  
RP SEQUENCE FROM N.A.  
RA Kitts P.;  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
RN [18]  
RP SEQUENCE FROM N.A.  
RA Schlieper D., von Wilcken-Bergmann B., Schmidt M., Sobek H.,  
RA Mueller-Hill B.;  
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: A BETA-LACTAM + H(2)O = A SUBSTITUTED BETA-

CC AMINO ACID.  
CC -!- SIMILARITY: THIS IS A CLASS-A BETA-LACTAMASE.  
DR EMBL; U36912; AAB39957.1; -  
DR EMBL; M74750; AAA24057.1; -  
DR EMBL; U36911; AAB39956.1; -  
DR EMBL; U31280; AAC44581.1; -  
DR EMBL; Y12694; CAA73226.1; -  
DR EMBL; U63018; AAC53676.1; -  
DR EMBL; U86815; AAB91427.1; -  
DR EMBL; U89327; AAB64384.1; -  
DR EMBL; U89329; AAB64387.1; -  
DR EMBL; U89330; AAB64389.1; -  
DR EMBL; A24782; CAA01735.1; -  
DR EMBL; U89331; AAB64391.1; -  
DR EMBL; U89672; AAB49980.1; -  
DR EMBL; AJ001614; CAA04868.1; -  
DR EMBL; U89332; AAB64392.1; -  
DR EMBL; U89333; AAB64394.1; -  
DR EMBL; U89334; AAB64395.1; -  
DR EMBL; U89335; AAB64398.1; -  
DR EMBL; U89337; AAB64401.1; -  
DR EMBL; U89338; AAB64403.1; -  
DR EMBL; U89339; AAB64405.1; -  
DR EMBL; U89940; AAB64407.1; -  
DR EMBL; U89671; AAB49977.1; -  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
DR GO; GO:0008800; F:beta-lactamase activity; IEA.  
DR GO; GO:0016787; F:hydrolase activity; IEA.  
DR GO; GO:0046677; P:response to antibiotic; IEA.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
KW Antibiotic resistance; Hydrolase; Plasmid; Signal.  
FT SIGNAL 1 23  
FT CHAIN 24 286 BETA-LACTAMASE II.  
FT SEQUENCE 286 AA; 31557 MW; 5EB2F2275375FA9 CRC64;  
SQ  
Query Match 98.9%; Score 1330; DB 2; Length 286;  
Best Local Similarity 98.9%; Pred. No. 4.3e-104;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HPETLVKVDADQLGARVGYIELDINSGEILESPRSERPPMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVDADQLGARVGYIELDINSKILSFRRERPEMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQIGRRIRHYSQNDIVVEYSPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRRIRHYSQNDIVVEYSPYTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143  
QY 121 KELTAPFLHMGDHYTRLDRWEPELNEAIPNDERDTTPVAMATLLRKLITGELLTLASRQ 180  
Db 144 KELTAPFLHMGDHYTRLDRWEPELNEAIPNDERDTTPVAMATLLRKLITGELLTLASRQ 203  
QY 181 QLIIDWMEADKYAGPLLRSALPAGWFLADKSGAGGRSGRTIAALGPDGKPSRIVVITTTG 240  
Db 204 QLIIDWMEADKYAGPLLRSALPAGWFLADKSGAGGRSGRTIAALGPDGKPSRIVVITTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286  
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ID Q38058 PRELIMINARY; PRT; 286 AA.  
AC Q38058;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, last annotation update)  
DE Beta lactamase.  
GN BLA.

OS Bacteriophage phi-X174.  
OC Viruses; ssDNA viruses; Microviridae; Microvirus.  
OX NCBI\_TaxID=10847;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95172401; PubMed=7867948;  
RA Henrich B., Schmidtberger B.;  
RT "A variant of phiX174 gene E-based positive selection vectors with  
enhanced lytic potential.";  
RL Gene 154:51-54(1995).  
DR EMBL; Z35638; CAA84692.1; -.  
DR PIR; S47061; S47061.  
DR HSSP; P00810; 1BTL.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31557 MW; 5EB2F22753375FA9 CRC64;

Query Match 98.9%; Score 1330; DB 9; Length 286;  
Best Local Similarity 98.9%; Pred. No. 4.3e-104;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSGEILSFRRSEERFPMSTFKVLLCGAVLSRID 60  
DB 24 HPETLVKVKDAEDQLGARVGYIELDLSGKILSFRRSEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
DB 84 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143  
QY 121 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 180  
DB 144 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITTTG 240  
DB 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
DB 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 3  
Q8KQ72 PRELIMINARY; PRT; 286 AA.  
AC Q8KQ72;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)  
DE Class A beta-lactamase TEM-106.  
GN BLATEM-106.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=YMC99/12/74;  
RA Yum J.H., Yong D., Shin J.H., Lee K., Chong Y.;  
RT "Characterization of a new extended-spectrum beta-lactamase (TEM-106)  
in an Escherichia coli clinical isolate in Korea.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY101578; AAM52207.1; -.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31484 MW; 137161BA6EF9AFB6 CRC64;

Query Match 98.7%; Score 1327; DB 2; Length 286;  
Best Local Similarity 98.1%; Pred. No. 7.8e-104;  
Matches 258; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSGEILSFRRSEERFPMSTFKVLLCGAVLSRID 60  
DB 24 HPETLVKVKDAEDQLGARVGYIELDLSGKILSFRRSEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
DB 84 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143  
QY 121 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 180  
DB 144 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITTTG 240  
DB 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
DB 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 4  
Q9R748 PRELIMINARY; PRT; 286 AA.  
AC Q9R748;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)  
DE Beta-lactamase class A (Fragment).  
GN BLATEM-20.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A268;  
RX MEDLINE=99216918; PubMed=10103213;  
RA Arlet G., Goussard S., Courvalin P., Philippon A.;  
RT "Sequence of the genes for TEM-20, TEM-21, TEM-22 and TEM-29 extended-  
spectrum beta-lactamases.";  
RT Antimicrob. Agents Chemother. 43:969-971(1999).  
RL Antimicrob. Agents Chemother. 43:969-971(1999).  
DR EMBL; Y17581; CAA76793.1; -.  
DR HSSP; P00810; ITEM.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
FT NON\_TER 286  
SQ SEQUENCE 286 AA; 31515 MW; 155F7CE493A16FB8 CRC64;

Query Match 98.5%; Score 1325; DB 2; Length 286;  
Best Local Similarity 98.1%; Pred. No. 1.1e-103;  
Matches 258; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSGEILSFRRSEERFPMSTFKVLLCGAVLSRID 60  
DB 24 HPETLVKVKDAEDQLGARVGYIELDLSGKILSFRRSEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
DB 84 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143  
QY 121 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 180  
DB 144 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDTTPVAMATTLRKLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITTTG 240

Db 204 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGASERGSRGIIAALGPDGKPSRIVIYTTG 263  
Qy 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 5

Q8KSD2 PRELIMINARY; PRT; 286 AA.  
AC Q8KSD2;  
DT 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)  
DE Beta-lactamase TEM-105.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Li J.-B., Li X., Yu X.-S.;  
RT "Cloning and pronucleus expression of the encoding gene of TEM-105  
RT type of beta-lactamases.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516720; AAM61953.1; -  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31542 MW; B3DE92C998C5A5EC CRC64;

Query Match 98.3%; Score 1322; DB 2; Length 286;  
Best Local Similarity 97.7%; Pred. No. 2.1e-103;  
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HPETLVKVDADQDLGARVGYIELDLNSGEILSFSEERFPMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVDADQDLGARVGYIELDLNSGEILSFSEERFPMSTFKVLLCGAVLSRD 83  
Qy 61 AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143  
Qy 121 KELTAFLNMGDHTRLDRWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFLNMGDHTRLDRWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
Qy 181 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGASERGSRGIIAALGPDGKPSRIVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGASERGSRGIIAALGPDGKPSRIVIYTTG 263  
Qy 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 6

034176 PRELIMINARY; PRT; 286 AA.  
AC 034176;  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Beta-lactamase TEM-43.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]

RP SEQUENCE OF 1-285 FROM N.A.  
RX MEDLINE=98325432; PubMed=9661002;  
RA Yang Y., Bhachech N., Bradford P.A., Uett B.D., Sahm D.F., Bush K.;  
RT "Ceftazidime-resistant Klebsiella pneumoniae and Escherichia coli  
RT isolates producing TEM-10 and TEM-43 beta-lactamases from St. Louis,  
RT Missouri.";  
RN Antimicrob. Agents Chemother. 42:1671-1676(1998).

[2]  
RP SEQUENCE FROM N.A.  
RA Yang Y., Bhachech N., Bradford P.A., Uett B.D., Sahm D.F., Bush K.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U95363; AAC32889.2; -  
DR HSSP; P00810; ITEM.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31465 MW; 1371745A6119B5B6 CRC64;

Query Match 98.3%; Score 1322; DB 2; Length 286;  
Best Local Similarity 97.7%; Pred. No. 2.1e-103;  
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HPETLVKVDADQDLGARVGYIELDLNSGEILSFSEERFPMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVDADQDLGARVGYIELDLNSGEILSFSEERFPMSTFKVLLCGAVLSRD 83  
Qy 61 AGQEQIGRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRIHYSONDLVYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGGP 143  
Qy 121 KELTAFLNMGDHTRLDRWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFLNMGDHTRLDRWEPELNEAI PNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
Qy 181 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGASERGSRGIIAALGPDGKPSRIVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLRLRSALPAGWFIADKSGASERGSRGIIAALGPDGKPSRIVIYTTG 263  
Qy 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 7

Q91AC0 PRELIMINARY; PRT; 286 AA.  
AC Q91AC0;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)  
DE Class A beta-lactamase.  
OS Proteus mirabilis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Proteus.  
OX NCBI\_TaxID=584;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PRM-1;  
RA Perilli M., Amicosante G.;  
RT "A new TEM ESBL highly active against cefotaxime in Proteus mirabilis  
RT clinical isolate.";  
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF143804; AAF66653.1; -  
DR HSSP; P00810; ITEM.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31514 MW; 8B437C51FC5D60A8 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;  
Best Local Similarity 97.7%; Pred. No. 2.5e-103;  
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGSKILESFRPEERFPMSTFKVLLCGAVLSRVD 83

QY 61 AGQEQIGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRRIHYSQNDLVKYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143

QY 121 KELTAFILHNMGDHYTRLDRMEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFILHNMGDHYTRLDRMEPELNEAIPNDERDTTPAAMATTLRKLLTGELLTLASRQ 203

QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVITYTG 240  
Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGASERGSRGIIITAAIGPDGKPSRIIVITYTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 8  
Q93A80 PRELIMINARY; PRT; 286 AA.  
ID Q93A80;  
AC Q93A80;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)  
DE Inhibitor-resistant beta-lactamase TEM-81.  
GN BLATEM-81.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20448741; PubMed=10991849;  
RA Leflon-Guibout V., Speldooren V., Heym B., Nicolas-Chanoine M.;  
RT "Epidemiological survey of amoxicillin-clavulanate resistance and  
RT corresponding molecular mechanisms in Escherichia coli isolates in  
RT France: new genetic features of bla(TEM) genes.";  
RL Antimicrob. Agents Chemother. 44:2709-2714(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Leflon-Guibout V., Speldooren V., Heym B., Nicolas-Chanoine M.-H.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF427127; AAL29433.1; -  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31483 MW; 582E34D2A08818F8 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;  
Best Local Similarity 97.3%; Pred. No. 2.5e-103;  
Matches 256; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGSKILESFRPEERFPMSTFKVLLCGAVLSRVD 83

QY 61 AGQEQIGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143

QY 121 KELTAFILHNMGDHYTRLDRMEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFILHNMGDHYTRLDRMEPELNEAIPNDERDTTPAAMATTLRKLLTGELLTLASRQ 203

QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVITYTG 240  
Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVITYTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 9  
Q9AGJ5 PRELIMINARY; PRT; 286 AA.  
ID Q9AGJ5  
AC Q9AGJ5;  
DT 01-JUN-2001 (Tremblrel. 17, Created)  
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Extended spectrum beta-lactamase TEM-63.  
GN BLATEM-63.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Hanson N.D., Moland E.S., Pitout J.D.;  
RT "TEM-63, A Novel TEM-type Extended Spectrum Beta-lactamase Expressed  
RT in Three Different Genera of Enterobacteriaceae from South Africa.";  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF332513; AAK17194.1; -  
DR HSSP; P00810; ITEM.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31449 MW; AEBB60086CE3AEB3 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;  
Best Local Similarity 97.7%; Pred. No. 2.5e-103;  
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGSKILESFRPEERFPMSTFKVLLCGAVLSRVD 83

QY 61 AGQEQIGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRRIHYSQNDLVKYSPTVEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143

QY 121 KELTAFILHNMGDHYTRLDRMEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFILHNMGDHYTRLDRMEPELNEAIPNDERDTTPAAMATTLRKLLTGELLTLASRQ 203

QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVITYTG 240  
Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIITAAIGPDGKPSRIIVITYTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 10  
Q9R435 PRELIMINARY; PRT; 286 AA.  
ID Q9R435  
AC Q9R435;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE EXTENDED SPECTRUM beta-lactamase.  
GN BLATEM-52.  
OS Klebsiella pneumoniae.

OG Plasmid pKK50-2.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KMK107;  
RA Cho D.T., Shin H.S.;  
RT "Molecular Evolution of blaTEM of Extended Spectrum of beta-lactamase (ESBL) in Klebsiella pneumoniae isolated in Korea.";  
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NEM865;  
RA Poyart C., Mugnier P., Quesnes G., Berche P., Trieu-Cuot P.;  
RT "A novel extended-spectrum TEM-type beta-lactamase from Klebsiella pneumoniae hydrolyzing Moxalactam.";  
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF027199; AAB84239.1; -.  
DR EMBL; Y13612; CAA73933.1; -.  
DR PDB; 1HTZ; 21-MAR-01.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
KW Plasmid.  
SQ SEQUENCE 286 AA; 31514 MW; 13717ACCB58F6FB6 CRC64;  
  
Query Match 98.2%; Score 1321; DB 2; Length 286;  
Best local Similarity 97.7%; Pred. No. 2.5e-103;  
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILSEFRSEERRPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRVD 83  
  
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRRIRHYSQNDLVKSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
  
QY 121 KELTAFILHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFILHNMGDHTVRLDRWEPELNEAIPNDERDTTPAAMATTLRKLLTGELLTLASRQ 203  
  
QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSRGIITAAALGPDGKPSRIVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGASERSRGIITAAALGPDGKPSRIVIYTTG 263  
  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286  
  
RESULT 11  
Q9RMS2 PRELIMINARY; PRT; 286 AA.  
AC Q9RMS2;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)  
DE Inhibitor-resistant beta-lactamase TEM-76.  
GN BLATEM-76.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20448741; PubMed=10991849;  
RA Leflon-Guibout V., Speldoren V., Heym B., Nicolas-Chanoine M.-H.;  
RT "Epidemiological survey of amoxicillin-clavulanate resistance and

RT corresponding molecular mechanisms in Escherichia coli isolates in  
RT france: new genetic features of bla(TEM) genes.";  
RL Antimicrob. Agents Chemother. 44:2709-2714(2000).  
DR EMBL; AF190694; AAF05613.1; -.  
DR HSSP; P00810; 1XPB.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31485 MW; 63BE4883A7055BD7 CRC64;  
  
Query Match 98.2%; Score 1321; DB 2; Length 286;  
Best local Similarity 97.7%; Pred. No. 2.5e-103;  
Matches 257; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILSEFRSEERRPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMSTFKVLLCGAVLSRVD 83  
  
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
  
QY 121 KELTAFILHNMGDHTVRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KELTAFILHNMGDHTVRLDRWEPELNEAIPNDERDTTPAAMATTLRKLLTGELLTLASRQ 203  
  
QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSRGIITAAALGPDGKPSRIVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSRGIITAAALGPDGKPSRIVIYTTG 263  
  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286  
  
RESULT 12  
Q8KMX4 PRELIMINARY; PRT; 286 AA.  
AC Q8KMX4;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, last annotation update)  
DE TEM-93 ES-beta-lactamase.  
GN BLA-TEM-93.  
OS Escherichia coli.  
OG Plasmid pblaTEM-93.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIS 3445/98;  
RA Gniadkowski M.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CLIS 3445/98;  
RA Gniadkowski M.;  
RT "Evolution of TEM extended-spectrum beta-lactamases in Poland.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ318093; CAC85660.1; -.  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
KW Plasmid.  
SQ SEQUENCE 286 AA; 31514 MW; 1555DCE499016FB8 CRC64;  
  
Query Match 98.2%; Score 1321; DB 2; Length 286;



Best Local Similarity 97.7%; Pred. No. 2.5e-103;  
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMMSTFKVLLCGAVLSRD 83  
QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
Db 84 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143  
QY 121 KELTSFLHNMGDHVTSLDRWEPELNEALPNDERDTTPVAMATTIRKLLTGELLTLASRQ 180  
Db 144 KELTSFLHNMGDHVTSLDRWEPELNEALPNDERDTTPVAMATTIRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGRIIAGPDGKPSRIIVITYTTG 240  
Db 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGRIIAGPDGKPSRIIVITYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 13

Q8KSD3 PRELIMINARY; PRT; 286 AA.  
AC Q8KSD3;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Beta-lactamase TEM-104.  
OS Klebsiella pneumoniae.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Klebsiella.  
OX NCBI\_TaxID=573;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Li J.-B., Li X., Yu Y.-S.;  
RT "Cloning and pronucleus expression of the encoding gene of TEM-104  
RT type of beta-lactamases.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF516719; AAM61952.1; -  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31543 MW; BB679BC8B18934B CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;  
Best Local Similarity 97.7%; Pred. No. 2.5e-103;  
Matches 257; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMMSTFKVLLCGAVLSRD 83  
QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
Db 84 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143  
QY 121 KELTSFLHNMGDHVTSLDRWEPELNEALPNDERDTTPVAMATTIRKLLTGELLTLASRQ 180  
Db 144 KELTSFLHNMGDHVTSLDRWEPELNEALPNDERDTTPVAMATTIRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGRIIAGPDGKPSRIIVITYTTG 240  
Db 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGRIIAGPDGKPSRIIVITYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 14

Q9RN48 PRELIMINARY; PRT; 286 AA.  
AC Q9RN48;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Beta-lactamase variant TEM-70.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SM91;  
RA Edelman M.V.;  
RT "Sequence diversity of the genes encoding broad-spectrum TEM-type  
RT beta-lactamases in clinical Escherichia coli strains.";  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF188199; AAF01046.1; -  
DR HSSP; P00810; 1XPB.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
FT VARIANT 202 Q -> R.  
SQ SEQUENCE 286 AA; 31487 MW; E864BA43B9776ED9 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;  
Best Local Similarity 97.7%; Pred. No. 2.5e-103;  
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMMSTFKVLLCGAVLSRD 83  
QY 61 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
Db 84 AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143  
QY 121 KELTSFLHNMGDHVTSLDRWEPELNEALPNDERDTTPVAMATTIRKLLTGELLTLASRQ 180  
Db 144 KELTSFLHNMGDHVTSLDRWEPELNEALPNDERDTTPVAMATTIRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGRIIAGPDGKPSRIIVITYTTG 240  
Db 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSGRIIAGPDGKPSRIIVITYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 15

Q32372 PRELIMINARY; PRT; 286 AA.  
ID Q32372;  
AC Q32372;  
DT 01-JAN-1998 (Tremblrel. 05, Created)  
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Beta-lactamase class A.  
GN BLA TEM-17.  
OS Capnocytophaga ochracea.  
OC Bacteria; Bacteroidetes; Flavobacteriia; Flavobacteriales;  
OC Flavobacteriaceae; Capnocytophaga.  
OX NCBI\_TaxID=1018;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20145403; PubMed=10681352;



RA Rosenau A., Cattier B., Gousset P., Harriau P., Philippon A.,  
RA Quentin R.;  
RT "Capnocytophaga ochracea: characterization of a plasmid-encoded  
RT extended-spectrum TEM-17 beta-lactamase in the phylum Flavobacter-  
RT Bacteroides.";  
RL Antimicrob. Agents Chemother. 44:760-762(2000).  
DR EMBL; Y14574; CAA74912.2; -.  
DR HSSP; P00810; 1XPB.  
DR InterPro; IPR001466; Beta\_lactamase.  
DR InterPro; IPR000871; Beta\_lactamase\_A.  
DR Pfam; PF00144; beta-lactamase; 1.  
DR PRINTS; PR00118; BLACTAMASEA.  
DR PROSITE; PS00146; BETA\_LACTAMASE\_A; 1.  
SQ SEQUENCE 286 AA; 31514 MW; BD498F6B9D369345 CRC64;

Query Match 98.2%; Score 1321; DB 2; Length 286;  
Best Local Similarity 97.7%; Pred. No. 2.5e-103;  
Matches 257; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGETLESFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDINSGETLESFRSEERFPMMSTFKVLLCGAVLSRD 83  
QY 61 AGQEQLGRRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTANLLTTIGGP 120  
Db 84 AGQEQLGRRRIHYSQNDLVKYSPTVEKHLTDGMTVRELCSAAITMSDNTANLLTTIGGP 143  
QY 121 KETLAFLNMGDHDVTRLDRWEPELNEAIPNDERDPTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KETLAFLNMGDHDVTRLDRWEPELNEAIPNDERDPTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKVAAGPLLRSALPAQWFIADKSGAGERGSRGIIAALGPDGKPSRIWVIYTTG 240  
Db 204 QLIDWMEADKVAAGPLLRSALPAQWFIADKSGAGERGSRGIIAALGPDGKPSRIWVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

Search completed: June 18, 2004, 19:10:01  
Job time : 47 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 18, 2004, 18:27:53 ; Search time 60 Seconds  
(without alignments)  
1238.500 Million cell updates/sec

Title: EPPER526106.PEP  
Perfect score: 1345  
Sequence: 1 hpetlvkvkdaedqigavg.....tmdermqiaiegaslikhw 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : A\_Geneseq\_29Jan04:\*
- 1: geneseqp1980s:\*
  - 2: geneseqp1990s:\*
  - 3: geneseqp2000s:\*
  - 4: geneseqp2001s:\*
  - 5: geneseqp2002s:\*
  - 6: geneseqp2003as:\*
  - 7: geneseqp2003bs:\*
  - 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	1330	98.9	263	AAE05544	Aae05544 E. coli m
2	1330	98.9	263	AAB36692	Aab36692 Escherich
3	1330	98.9	264	AAW16634	Aaw16634 Beta-lact
4	1330	98.9	264	AAW18680	Aaw18680 Intracell
5	1330	98.9	286	AAK31575	Aar31575 Ampicilli
6	1330	98.9	286	AAK97619	Aar97619 Secretory
7	1330	98.9	286	AAK96423	Aar96423 Cytochrom
8	1330	98.9	286	AAW16635	Aaw16635 Beta-lact
9	1330	98.9	286	AAW18679	Aaw18679 Secretory
10	1330	98.9	286	AAW08529	Aay08529 Vector pA
11	1330	98.9	286	AAW10442	Aab10442 Expressio
12	1330	98.9	286	AAW10438	Aab10438 Expressio
13	1330	98.9	286	AAW10440	Aab10440 Expressio
14	1330	98.9	286	AAW50898	Aab50898 Protein e
15	1330	98.9	286	AAW31173	Aab31173 Amino aci
16	1330	98.9	286	AAU75551	Aau75551 celZ inte
17	1330	98.9	286	ABP55474	Abp55474 Vector pc
18	1330	98.9	286	ABR43622	Abi43622 Cloning v
19	1330	98.9	290	AAU23219	Aau23219 Novel hum
20	1330	98.9	290	AAW84362	Aam84362 Human imm
21	1330	98.9	327	AAW16636	Aaw16636 Beta-lact
22	1330	98.9	327	AAW18681	Aaw18681 Membrane-
23	1330	98.9	408	ABR55981	Abi55981 hCG beta-
24	1330	98.9	585	ADA67747	Ada67747 Beta-lact
25	1330	98.9	1088	AAK88636	Aar88636 Plasmid p

26	1330	98.9	1277	2	AAK52701	Aar52701 Plasmid p
27	1330	98.9	2307	3	AAW70064	Aay70064 Recombina
28	1330	98.9	2307	3	AAW70066	Aay70066 Recombina
29	1329	98.8	286	2	AAW06551	Aay06551 Escherich
30	1329	98.8	1293	7	ADC22811	Adc22811 Human G p
31	1329	98.8	1967	6	ABB82793	Abb82793 Amino aci
32	1325	98.5	265	2	AAW08234	Aay08234 E. coli R
33	1325	98.5	265	2	AAW08232	Aay08232 E. coli R
34	1325	98.5	265	2	AAW48613	Aaw48613 Escherich
35	1325	98.5	265	2	AAW49892	Aay49892 RTM with
36	1325	98.5	265	2	AAW49890	Aay49890 Escherich
37	1325	98.5	265	4	AAE06924	Aae06924 E. coli T
38	1325	98.5	265	4	AAE06922	Aae06922 E. coli T
39	1325	98.5	265	5	AAW51111	Aam51111 Escherich
40	1325	98.5	283	4	AAW62272	Aab62272 Heavy cha
41	1325	98.5	285	5	AAW51112	Aam51112 Escherich
42	1325	98.5	286	1	AAW90058	Aap90058 beta-lact
43	1325	98.5	286	2	AAW08233	Aay08233 E. coli R
44	1325	98.5	286	2	AAW48614	Aaw48614 Escherich
45	1325	98.5	286	2	AAW80733	Aaw80733 Amino aci

ALIGNMENTS

RESULT 1	
AAE05544	AAE05544 standard; protein; 263 AA.
XX	
AC	AAE05544;
XX	
DT	24-SEP-2001 (first entry)
XX	
DE	E. coli mature TEM-1 beta-lactamase.
XX	
KW	Interaction-dependent enzyme association, IdHA system; biosensor;
KW	circularly permuted interaction-activated protein; marker protein;
KW	type A beta-lactamase; TEM-1 beta-lactamase; protein-protein interaction;
KW	therapeutic; drug screening; thioredoxin; ampicillin resistance.
XX	
OS	Escherichia coli.
XX	
FH	Key
FT	Cleavage-site
FT	Location/Qualifiers
FT	/note= "Break-point between alpha and omega fragments"
FT	36.40
FT	/note= "Inter-sub-domain loop"
FT	38.39
FT	/note= "Break-point between alpha and omega fragments"
FT	45
FT	/note= "Break-point between alpha and omega fragments"
FT	74.75
FT	/note= "Break-point between alpha and omega fragments"
FT	149.150
FT	/note= "Break-point between alpha and omega fragments"
FT	172.173
FT	/note= "Break-point between alpha and omega fragments"
FT	189.204
FT	/note= "Break-point between alpha and omega fragments"
FT	190.191
FT	/note= "Break-point between alpha and omega fragments"
FT	202.203
FT	/note= "Break-point between alpha and omega fragments"
FT	228.229
FT	/note= "Break-point between alpha and omega fragments"
PN	WO200151629-A2.
XX	
PD	19-JUL-2001.
XX	
PF	16-JAN-2001; 2001WO-US001651.
XX	
PR	13-JAN-2000; 2000US-0175968P.
PR	15-MAR-2000; 2000US-00526106.

XX (PANO-) PANORAMA RES INC.  
PA Balint RF, Her J;  
XX WPI; 2001-451857/48.  
XX N-PSDB; AAD10411.  
DR  
XX  
XX  
PT Interaction-dependent enzyme association systems for detecting  
PT interactions between two or three polypeptides, especially in human  
PT therapeutics, diagnostics or prognostics, comprise circularly permuted  
PT proteins.  
XX  
XX Claim 38; Fig 2; 104pp; English.  
PS  
XX  
XX The invention relates to new interaction-dependent enzyme association  
CC (IDEA) systems that comprise a fusion sequence that encodes for a  
CC circularly permuted, interaction-activated proteins that reassemble to  
CC form functionally reconstituted marker proteins which produce a  
CC detectable signal upon the association of two oligopeptides, or upon  
CC simultaneous association of two oligopeptides with a third oligopeptide.  
CC The marker protein is preferably a type A beta-lactamase, especially TEM-  
CC 1 beta-lactamase of Escherichia coli. The oligopeptide is a member of a  
CC proteome library selected from single chain antibody Fv fragment library,  
CC an antibody light chain variable region library and a peptide library  
CC displayed within thioredoxin. The IDEA systems are useful for detecting  
CC and identifying interactions between intracellular as well as  
CC extracellular proteins, particularly between two or three polypeptides.  
CC The systems are also useful in selecting with a single marker protein the  
CC incorporation of multiple genetic traits in a host cell. In particular,  
CC the systems are useful in many applications in human therapeutics,  
CC diagnostics and prognostics, as well as in high-throughput screening  
CC systems for the discovery and validation of pharmaceutical targets and  
CC drugs. Prior systems (e.g. E. coli Dimer Detection System, Yeast two-  
CC hybrid system or Selective Infective Phage System) require multiple steps  
CC between interaction and phenotype, which cause severe loss of efficiency  
CC due to high false positive and false negative rates. The present system  
CC is capable of simultaneous detection of multiple interactions between  
CC extra-cellular as well as intracellular proteins in a high throughput  
CC format. The circularly permuted marker proteins comprising interaction-  
CC dependent enzymes find use in cell-based sensors for activation or  
CC inhibition of metabolic or signal transduction pathways, in high-  
CC throughput mapping of pair-wise protein-protein interactions within and  
CC between the proteomes of cells, tissues and pathogenic organisms, and in  
CC cell-based screens for high-throughput selection of inhibitors of any  
CC protein-protein interaction. The present sequence is Escherichia coli  
CC mature TEM-1 beta-lactamase enzyme from plasmid pBR322. TEM-1 beta-  
CC lactamase is a product of ampicillin resistance gene. The enzyme has two  
CC domains, alpha-omega and mu  
XX  
XX Sequence 263 AA;  
SQ  
Query Match 98.9%; Score 1330; DB 4; Length 263;  
Best Local Similarity 98.9%; Pred. No. 1.9e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMNSTFKVLLCGAVLSRID 60  
DB 1 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMNSTFKVLLCGAVLSRID 60  
QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
DB 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
QY 121 KETLTAFLHNMGDHVTIRLDKRWEPNELNEATPNDERDTTPVAMATTLRKLLTGEILLTASRQ 180  
DB 121 KETLTAFLHNMGDHVTIRLDKRWEPNELNEATPNDERDTTPVAMATTLRKLLTGEILLTASRQ 180  
QY 181 QLIDWMEADKAVGELLRSALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVVITTTG 240  
DB 181 QLIDWMEADKAVGELLRSALPAGWFIADKSGAGERSGRTIAALGPDGKPSRIVVITTTG 240  
QY 241 SQATMDERNRQIAETIGASLIKHW 263

DB 241 SQATMDERNRQIAETIGASLIKHW 263  
RESULT 2  
AAB36692  
ID AAB36692 standard; protein; 263 AA.  
XX AAB36692;  
AC  
XX  
DT 15-MAR-2001 (first entry)  
XX  
DE Escherichia coli mature TEM-1 beta-lactamase protein sequence.  
XX  
KM Interaction-activated protein; beta-lactamase; protein interaction.  
XX  
OS Escherichia coli.  
XX  
PN WO200071702-A1.  
XX  
PD 30-NOV-2000.  
XX  
PF 16-MAR-2000; 2000WO-US007108.  
XX  
PR 25-MAY-1999; 99US-0135926P.  
PR 13-JAN-2000; 2000US-0175968P.  
XX  
PA (PANO-) PANORAMA RES INC.  
XX  
PI Balint RF, Her J;  
XX  
DR WPI; 2001-032034/04.  
DR N-PSDB; AAC90773.  
XX  
XX Novel fragment complementation system to identify interactions between  
PT polypeptides comprises fragment pairs having first and second members  
PT that reassemble into a marker protein which has a directly detectable  
PT signal.  
XX  
PS Disclosure; Fig 2; 94pp; English.  
XX  
XX The present invention describes a fragment complementation system (I)  
CC which comprises a first oligopeptide (OP1) containing an N-terminal  
CC fragment with a C-terminal break point and a second oligopeptide (OP2)  
CC comprising a C-terminal with a N-terminal breakpoint, in which the C and  
CC N terminal fragments are both derived from a marker protein (MP) and  
CC reassemble to form a functionally reconstituted MP. Methods from the  
CC present invention are used for monitoring the occurrence of protein-  
CC protein interactions in a sample, identifying oligopeptide interactions  
CC between two different proteomes, identifying epitopes that bind to an  
CC immunoglobulin (Ig) variable region, for identifying interactions between  
CC an extracellular domain of a transmembrane protein and a polypeptide, for  
CC high-throughput identification of compounds that inhibit phosphorylation-  
CC regulated signal transducers, forming a enzyme complementation system for  
CC selecting simultaneous incorporation of multiple genetic elements into a  
CC host cell and for activating a beta-lactam derivative of an antitumour  
CC compound in a host who is in need of it. The present sequence represents  
CC the Escherichia coli mature TEM-1 beta-lactamase, which is used in the  
CC exemplification of the present invention  
XX  
XX Sequence 263 AA;  
SQ  
Query Match 98.9%; Score 1330; DB 4; Length 263;  
Best Local Similarity 98.9%; Pred. No. 1.9e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMNSTFKVLLCGAVLSRID 60  
DB 1 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMNSTFKVLLCGAVLSRID 60  
QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
DB 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120

QY 121 KELTSFLHNMGDHVTRLDRWEPELNEAI PNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 121 KELTSFLHNMGDHVTRLDRWEPELNEAI PNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180  
QY 181 QLIDWMEADKVA GPELLRSALPAGWFIADKSGAGERSRGITIAALGPDGKPSRIVVIYTTG 240  
Db 181 QLIDWMEADKVA GPELLRSALPAGWFIADKSGAGERSRGITIAALGPDGKPSRIVVIYTTG 240  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 241 SQATMDERNRQIAEIGASLIKHW 263

## RESULT 3

AAW16634  
ID AAW16634 standard; protein; 264 AA.

AC AAW16634;

DT 09-AUG-1997 (first entry)

DE Beta-lactamase (including signal peptide).

KW Gene directed enzyme prodnug therapy; GDEPT;  
KW virus directed enzyme prodnug therapy; VDEPT; beta-lactamase; cancer;  
KM HIV; inflammation.

OS Escherichia coli.

FT Key Location/Qualifiers  
1..23  
/label= Sig\_peptide

PN WO9719180-A2.

PD 29-MAY-1997.

PF 19-NOV-1996; 96WO-GB002845.

PR 20-NOV-1995; 95GB-00023703.

PA (GLAXO ) GLAXO GROUP LTD.

PI Dev I, Moore JT, Ohmstede C;

DR WPI; 1997-298117/27.

DR N-PSDB; AAT66736.

PT Molecular chimaera for gene or virus directed enzyme prodnug therapy -  
useful for treatment of cancer, viral infection or inflammation.

PS Example; Page 28; 38pp; English.

CC Escherichia coli beta-lactamase (AAW16634), including the signal peptide,  
is the expression product of a molecular chimaera, designated pCMV-BL  
(AAT66737), in which the beta-lactamase gene is under control of the CMV  
intermediate/early promoter. Vectors consisting of a transcriptional  
regulatory DNA sequence linked to a beta-lactamase gene can be used for  
enzyme prodnug therapy. Expression of the beta-lactamase in a targeted  
cell allows conversion of a prodnug into an agent toxic to the cell for  
treatment of cancer, viral (e.g. HIV) infection or inflammation.  
CC Secretion of the enzyme has the advantage of increasing neighbouring cell  
kill

XX Sequence 264 AA;

QY Query Match 98.9%; Score 1330; DB 2; Length 264;  
Best Local Similarity 98.9%; Pred. No. 1.9e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 HPETLVKVKDAEDQLGARVGYIELDLNSGILESFRSEERFPMMSTFKVLLCGAVLSRID 60  
|||||

Db 2 HPETLVKVKDAEDQLGARVGYIELDLNSGILESFRSEERFPMMSTFKVLLCGAVLSRID 61  
QY 61 AGQEQLRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 62 AGQEQLRRIHYSONDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 121  
QY 121 KELTSFLHNMGDHVTRLDRWEPELNEAI PNDERDTTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 122 KELTSFLHNMGDHVTRLDRWEPELNEAI PNDERDTTTPVAMATTLRKLLTGELLTLASRQ 181  
QY 181 QLIDWMEADKVA GPELLRSALPAGWFIADKSGAGERSRGITIAALGPDGKPSRIVVIYTTG 240  
Db 182 QLIDWMEADKVA GPELLRSALPAGWFIADKSGAGERSRGITIAALGPDGKPSRIVVIYTTG 241  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 242 SQATMDERNRQIAEIGASLIKHW 264

## RESULT 4

AAW18680  
ID AAW18680 standard; protein; 264 AA.

AC AAW18680;

DT 13-AUG-1997 (first entry)

DE Intracellularly-expressed beta-lactamase.

KW Prodnug therapy; gene directed enzyme prodnug therapy; GDEPT;  
KW virus directed enzyme prodnug therapy; VDEPT; lung cancer;  
KM beta-lactamase; pCMV-delBL.

OS Escherichia coli.

PN WO9719183-A2.

PD 29-MAY-1997.

PF 19-NOV-1996; 96WO-GB002846.

PR 20-NOV-1995; 95GB-00023703.

PA (GLAXO ) GLAXO GROUP LTD.

PI Dev I, Moore JT, Sethna PB;

DR WPI; 1997-298118/27.

DR N-PSDB; AAT70311.

PT DNA construct for gene-directed enzyme prodnug therapy of lung cancer -  
comprises lung- or neuroendocrine-specific promoter controlling  
expression of prodnug-converting enzyme.

PS Example 811; Page 32-34; 53pp; English.

CC The intracellular form (AAW18680) of TEM beta-lactamase is expressed by  
pCMV-delBL (AAT70311) in which a PCR-amplified beta-lactamase coding  
sequence, minus the signal sequence, is placed under control of the  
intermediate/early promoter of cytomegalovirus. Intracellular beta-  
lactamase constructs, placed under control of promoter/enhancer elements  
of lung-associated protein or neuroendocrine marker protein genes, can be  
used in novel chimaeric molecules for use in prodnug therapy of lung  
cancer

XX Sequence 264 AA;

QY Query Match 98.9%; Score 1330; DB 2; Length 264;  
Best Local Similarity 98.9%; Pred. No. 1.9e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 HPETLVKVKDAEDQLGARVGYIELDLNSGILESFRSEERFPMMSTFKVLLCGAVLSRID 60  
|||||

Db	2	HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMWSTFKVLLCGAVLSRID	61
QY	61	AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMIVRELCSAAITMSDNTAANLLTTIGSP	120
Db	62	AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMIVRELCSAAITMSDNTAANLLTTIGSP	121
QY	121	KELTAFLHNMGDHVTIRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ	180
Db	122	KELTAFLHNMGDHVTIRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ	181
QY	181	QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG	240
Db	182	QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG	241
QY	241	SOATMDERNRQIAEIGASLIKHW	263
Db	242	SOATMDERNRQIAEIGASLIKHW	264

RESULT 5  
AAR31575  
ID AAR31575 standard; protein; 286 AA.

AC AAR31575;  
XX  
XX 10-MAR-2003 (revised)  
DT 04-JUN-1993 (first entry)  
XX  
XX Ampicillin resistance protein.  
DE  
XX  
XX CYP1A1; PRNH127; PRNH155; xeroderma pigmentosum group A; XPA;  
KW xenobiotics; circular; chimeric cytochrome P450IA1.  
XX

OS Homo sapiens.  
XX  
XX US5180666-A.  
PN  
XX  
XX 19-JAN-1993.  
PD  
XX  
XX 27-JUN-1991; 91US-00721775.  
PF  
XX  
XX 27-JUN-1991; 91US-00721775.  
PR  
XX  
XX 27-JUN-1991; 91US-00721775.  
PA (UYWA-) UNIV WAYNE STATE.  
PI  
XX  
XX States JC, Hines RN, Novak RF;  
PI  
XX  
XX WPI; 1993-052845/06.  
DR  
XX  
XX N-PSDB; AAQ36498.

XX  
XX  
XX In vitro method for testing mutagenicity of a chemical - by metabolising  
PT chemical cell line consisting of transformed fibroblasts having  
PT detectable cytochrome P450 mixed function oxidase activity and detecting  
PT gene damage.  
XX

PS Disclosure; Col 21-24; 24pp; English.

XX  
XX  
XX The expression constructs PRNH127 and PRNH155 contain identical sequences  
CC but were constructed using different strategies (see AAQ36498). The  
CC constructs comprise exons 2-7 of human CYP1A1 gene under the control of  
CC the inducible mouse metallothionein (MMT-1) promoter. The constructs also  
CC contain an open reading frame in the opposite orientation to the  
CC cytochrome P450 exons. This ORF encodes ampicillin resistance. The  
CC constructs are suitable for transformation of human fibroblasts derived  
CC from the xeroderma pigmentosum group A. Cultures of the transformed  
CC fibroblasts can be used to test substances for mutagenicity. The presence  
CC of the inducible cytochrome P450 gene allows metabolism of the substance  
CC to mutagenic metabolites. (Updated on 10-MAR-2003 to add missing OS  
CC field.)  
XX  
XX

SQ Sequence 286 AA;

Query Match 98.9%; Score 1330; DB 2; Length 286;

Best Local Similarity 98.9%; Pred. No. 2.2e-129;				
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;				
QY	1	HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRSEERFPMWSTFKVLLCGAVLSRID	60	
Db	24	HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMWSTFKVLLCGAVLSRID	83	
QY	61	AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMIVRELCSAAITMSDNTAANLLTTIGSP	120	
Db	84	AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMIVRELCSAAITMSDNTAANLLTTIGSP	143	
QY	121	KELTAFLHNMGDHVTIRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ	180	
Db	144	KELTAFLHNMGDHVTIRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ	203	
QY	181	QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG	240	
Db	204	QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVIYTTG	263	
QY	241	SOATMDERNRQIAEIGASLIKHW	263	
Db	264	SOATMDERNRQIAEIGASLIKHW	286	

RESULT 6  
AAR97619  
ID AAR97619 standard; protein; 286 AA.

AC AAR97619;  
XX  
XX 20-AUG-1996 (first entry)  
DT  
XX  
XX Secretory beta-lactamase.  
DE

XX  
XX Gene therapy; gene directed enzyme prodnug therapy; GDEPT;  
KW virus directed enzyme prodnug therapy; VDEPT; prodnug activation;  
KW cytotoxic; cytostatic; cancer; tumour; retrovirus; vector;  
KW beta-lactamase; cephalosporin.  
XX

XX Synthetic.

OS  
XX  
XX WO9616179-A1.  
PN  
XX  
XX 30-MAY-1996.  
PD  
XX  
XX 20-NOV-1995; 95WO-GB002716.  
PF  
XX  
XX 18-NOV-1994; 94GB-00023367.  
PR  
XX  
XX (WELL ) WELLCOME FOUND LTD.  
PA

XX  
XX Dev IK, Moore JT, Ohmstede C;  
PI  
XX  
XX WPI; 1996-268615/27.  
DR  
XX  
XX N-PSDB; AAT29220.

XX  
XX  
XX Molecular chimera for use in enzyme gene therapy - is activated in a  
PT target cell to express a secretable enzyme which cleaves a prodnug  
PT outside the cell into a cytotoxic or cytostatic agent.  
XX

PS Example 3; Page 57-58; 73pp; English.

XX  
XX  
XX A secretory beta-lactamase (AAR97619) is expressed from DNA construct  
CC pCMV-BL (AAT29220), in which the beta-lactamase coding sequence is under  
CC the control of the intermediate/early cytomegalovirus promoter. Beta-  
CC lactamase delivery to mammalian cells confers sensitivity to  
CC cephalosporin prodnugs. Liposomal DNA/5-fluorouracil prodnug combinations  
CC resulted in s.c. tumour regression in mice bearing A549 tumours. Survival  
CC of mice bearing human large cell lung H460 intrathoracic (i.t.) tumours  
CC was increased upon i.t. injection of the secretory beta-lactamase DNA  
CC construct.  
XX  
XX

SQ Sequence 286 AA;

Query Match 98.9%; Score 1330; DB 2; Length 286;  
Best Local Similarity 98.9%; Pred. No. 2.2e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRPEERFPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQIGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
Db 84 AGQEQIGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143

QY 121 KETLAFLEHMGDHYTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KETLAFLEHMGDHYTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203

QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIVITYTTG 240  
Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIVITYTTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 7  
AAR96423  
ID AAR96423 standard; protein; 286 AA.  
XX  
AC AAR96423;  
XX  
DT 25-MAR-2003 (revised)  
DT 25-NOV-1996 (first entry)  
XX  
DE Cytochrome P450 (CYP1A1 construct).  
XX  
KM cytochrome; P450; metallothionein; mouse; human; cytotoxicity; assay;  
KM metabolism.  
XX  
OS Homo sapiens.  
XX  
PN US5525482-A.  
XX  
PD 11-JUN-1996.  
XX  
PF 15-NOV-1994; 94US-00339658.  
XX  
PR 27-JUN-1991; 91US-00721775.  
PR 09-DEC-1992; 92US-00990295.  
XX  
PA (UYMA-) UNIV WAYNE STATE.  
XX  
PI Hines RN, Novak RF, States JC;  
XX  
DR WPI; 1996-286397/29.  
DR N-PSDB; AAT30354.  
XX  
XX  
PT Testing chemicals for cytotoxicity to human by detecting gene damage -  
PT using recombinant fibroblasts transformed with cytochrome P450 gene under  
PT control of inducible promoter.  
XX  
PS Disclosure; Col 17-24; 26pp; English.  
XX  
CC The present sequence is encoded by a chimeric mouse metallothionein-  
CC cytochrome P450IA1 (CYP1A1) expression construct. Two clones, PRNH127 and  
CC PRNH15, were isolated by different methods and which both had the same  
CC sequence. The CYP1A1 construct is used in assays to test for cytotoxicity  
CC of humans to a chemical. The method comprises exposing human fibroblast  
CC cells normally not including any cytochrome P450 activity to potentially  
CC toxic chemicals. The cells having been transformed to express cytochrome  
CC P450, under the control of a controllable promoter through the CYP1A1  
CC gene, upon exposure to the chemical in vitro. The chemical is metabolised

CC intracellularly into a cytochrome metabolite by oxidation within the  
CC fibroblasts through the intracellular cytochrome P450 mixed function  
CC oxidase enzymes expressed by the cells. Gene damage in the test cells is  
CC detected as an indication of cytotoxicity of the chemical. (Updated on 25  
CC -MAR-2003 to correct PF field.)  
XX  
SQ Sequence 286 AA;

Query Match 98.9%; Score 1330; DB 2; Length 286;  
Best Local Similarity 98.9%; Pred. No. 2.2e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRPEERFPMSTFKVLLCGAVLSRID 83

QY 61 AGQEQIGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 120  
Db 84 AGQEQIGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSP 143

QY 121 KETLAFLEHMGDHYTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db 144 KETLAFLEHMGDHYTRLDRWEPELNEAIPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203

QY 181 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIVITYTTG 240  
Db 204 QLIDWMEADKVAAGPLLRSALPAGWFIADKSGAGERSGRIIALGPDGKPSRIVITYTTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 8  
AAW16635  
ID AAW16635 standard; protein; 286 AA.  
XX  
AC AAW16635;  
XX  
DT 09-AUG-1997 (first entry)  
XX  
DE Beta-lactamase (no signal peptide).  
XX  
KM Gene directed enzyme prodnug therapy; GDEPT;  
KM virus directed enzyme prodnug therapy; VDEPT; beta-lactamase; cancer;  
KM HIV; inflammation.  
XX  
OS Escherichia coli.  
XX  
PN WO9719180-A2.  
XX  
PD 29-MAY-1997.  
XX  
PF 19-NOV-1996; 96WO-GB002845.  
XX  
PR 20-NOV-1995; 95GB-00023703.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Dev I, Moore JT, Ohmstede C;  
XX  
DR WPI; 1997-298117/27.  
DR N-PSDB; AAT66737.  
XX  
XX  
PT Molecular chimaera for gene or virus directed enzyme prodnug therapy -  
PT useful for treatment of cancer, viral infection or inflammation.  
XX  
PS Example; Page 26; 38pp; English.  
XX  
CC Escherichia coli beta-lactamase (AAW16635), lacking the signal peptide,  
CC is the expression product of a molecular chimaera, designated pcMV-delBL  
CC (AAT66738), in which the beta-lactamase gene is under control of the CMV  
CC intermediate/early promoter. Vectors consisting of a transcriptional



CC regulatory DNA sequence linked to a beta-lactamase gene can be used for  
CC enzyme prodrg therapy. Intracellular expression of the beta-lactamase in  
CC a targeted cell allows conversion of a prodrg into an agent toxic to  
CC the cell for treatment of cancer, viral (e.g. HIV) infection or  
CC inflammation

XX Sequence 286 AA;

Query Match 98.9%; Score 1330; DB 2; Length 286;  
Best Local Similarity 98.9%; Pred. No. 2.2e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSRSEERFPMMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTANLLLTIGGP 120  
Db 84 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTANLLLTIGGP 143  
QY 121 KELTAFILNMGDHVTIRLDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 180  
Db 144 KELTAFILNMGDHVTIRLDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 203  
QY 181 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGGIIAALGPDGKPSRIWIYTTG 240  
Db 204 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGGIIAALGPDGKPSRIWIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 9  
AAW18679  
ID AAW18679 standard; protein; 286 AA.

XX AAW18679;

DT 13-AUG-1997 (first entry)

DE Secretory beta-lactamase.

XX Prodrug therapy; gene directed enzyme prodrg therapy; GDEPT;  
KM virus directed enzyme prodrg therapy; VDEPT; lung cancer;  
KM beta-lactamase; pCMV-BL.

XX Escherichia coli.

OS  
XX  
EH Key Location/Qualifiers  
FT Peptide 1..23  
FT /label= Sig\_peptide  
FT 24..286  
FT Protein /label= Mat\_protein

XX WO9719183-A2.

XX 29-MAY-1997.

XX 19-NOV-1996; 96WO-GB002846.

XX 20-NOV-1995; 95GB-00023703.

XX (GLAX ) GLAXO GROUP LTD.

XX Dev I, Moore JT, Sethna PB;

XX WPI; 1997-298118/27.

DR N-PSDB; AAT70309.

XX DNA construct for gene-directed enzyme prodrg therapy of lung cancer -  
PT comprises lung- or neuroendocrine-specific promoter controlling  
PT expression of prodrg-converting enzyme.

XX Example 8ii; Page 26-27; 53pp; English.

PS The secreted form (AAW18679) of TEM beta-lactamase is expressed by pCMV-  
XX BL (AAT70309) in which a PCR-amplified beta-lactamase coding sequence is  
CC placed under control of the intermediate/early promoter of  
CC cytomegalovirus. Secretory beta-lactamase constructs, placed under  
CC control of promoter/enhancer elements of lung- associated protein or  
CC neuroendocrine marker protein genes, can be used in novel chimaeric  
CC molecules for use in prodrg therapy of lung cancer

XX Sequence 286 AA;

Query Match 98.9%; Score 1330; DB 2; Length 286;  
Best Local Similarity 98.9%; Pred. No. 2.2e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSRSEERFPMMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSRSEERFPMMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTANLLLTIGGP 120  
Db 84 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTANLLLTIGGP 143  
QY 121 KELTAFILNMGDHVTIRLDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 180  
Db 144 KELTAFILNMGDHVTIRLDWEPELNEAIPNDERDITTPVAMATTLRKLTGELLTLASRQ 203  
QY 181 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGGIIAALGPDGKPSRIWIYTTG 240  
Db 204 QLIDMMEADKVAGPLLRSLPAGWFIADKSGAGERSGGIIAALGPDGKPSRIWIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 10  
AAV08529  
ID AAV08529 standard; protein; 286 AA.

XX AAV08529;

DT 03-AUG-1999 (first entry)

DE Vector pASK75 beta-la protein.

XX Firefly; luciferase; tetracycline; transcriptional control; TetR; TetA;  
KM tetracycline repressor; tetracycline promoter; luxCDABE;  
KM insect; Tn10; medicine; dosage; cheese production; antibiotic; foodstuff;  
KM allergy.

XX Synthetic.

XX WO9925866-A1.

XX 27-MAY-1999.

XX 11-NOV-1998; 98WO-FI000873.

XX 14-NOV-1997; 97FI-00004235.

XX (KORP/) Korpela M.

XX (KARP/) Karp M.

XX (KURI/) Kurittu J.

PI Korpela M, Karp M, Kurittu J;

XX WPI; 1999-338015/28.

DR N-PSDB; AAV72418.

XX Assaying for tetracycline using recombinant prokaryotic cells.



PN DE19900635-A1.  
XX  
PD 13-JUL-2000.  
XX  
PF 11-JAN-1999; 99DE-01000635.  
XX  
PR 11-JAN-1999; 99DE-01000635.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Breitling F, Poustka A, Moldenhauer G;  
XX  
DR MPI; 2000-499832/45.  
DR N-PSDB; AAA71428.  
XX  
PT Selecting monoclonal antibodies, by expressing them on the surface of  
PT hybridomas attached to antibody-binding protein, then reaction with  
PT antibody library.  
XX  
PS Claim 16; Fig 1; 22pp; German.  
XX  
CC This invention describes a novel method for the selection of monoclonal  
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma  
CC cells to produce antibody-producing hybridomas such that the antibodies  
CC are presented at the surface of the hybridomas by an antibody-binding  
CC protein (I); and (ii) binding the antibody to antigens (Ag). The  
CC invention also describes antibody-binding proteins (I) that comprise a  
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa  
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)  
CC molecule; an antibody-binding site of proteins A, G, L or Ig, and the  
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)  
CC or CD52. The method is used to select Mab with specificity for particular  
CC antigens. Mab can be selected without separate culture of hybridomas, and  
CC selection can be made against many antigens in a library, optionally on  
CC the basis of strength of affinity for a particular antigen. Complex  
CC mixtures of hybridomas can be used for selection, reducing the time and  
CC cost involved in Mab selection. This sequence represents the Neo-R  
CC protein contained in the expression vector pSEX114 which contains the  
CC bla protein, Neo-R and protein G described in the method of the invention  
XX  
SQ Sequence 286 AA;  
Query Match 98.9%; Score 1330; DB 3; Length 286;  
Best Local Similarity 98.9%; Pred. No. 2.2e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGEILLESFRSEERPEPMSTFKVLLCGAVLSRID 60  
Db HPE TLVKVDAEDQLGARVGYIELDINSGEILLESFRSEERPEPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KELTSALFNMGDHTVRLDRWEPELNEALPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db KELTSALFNMGDHTVRLDRWEPELNEALPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKYAGPLLRSALPAGWFIADKSGAGERGSRGIITAAIGPDGKPSRIIVITYTTG 240  
Db QLIDWMEADKYAGPLLRSALPAGWFIADKSGAGERGSRGIITAAIGPDGKPSRIIVITYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db SQATMDERNRQIAEIGASLIKHW 266  
RESULT 13  
AAB10440  
ID AAB10440 standard; protein; 286 AA.  
XX  
AC AAB10440;  
XX

DT 01-DEC-2000 (first entry)  
XX  
DE Expression vector pSEX11G2 bla protein.  
XX  
KW Expression vector; antibody binding protein; monoclonal antibody; Neo-R;  
KW B lymphocyte; myeloma cell; hybridoma; protein G; bla protein.  
XX  
OS Synthetic.  
XX  
PN DE19900635-A1.  
XX  
PD 13-JUL-2000.  
XX  
PF 11-JAN-1999; 99DE-01000635.  
XX  
PR 11-JAN-1999; 99DE-01000635.  
XX  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX  
PI Breitling F, Poustka A, Moldenhauer G;  
XX  
DR MPI; 2000-499832/45.  
DR N-PSDB; AAA71429.  
XX  
PT Selecting monoclonal antibodies, by expressing them on the surface of  
PT hybridomas attached to antibody-binding protein, then reaction with  
PT antibody library.  
XX  
PS Claim 16; Fig 2; 22pp; German.  
XX  
CC This invention describes a novel method for the selection of monoclonal  
CC antibodies (Mab) which comprises (i) fusing B lymphocytes with myeloma  
CC cells to produce antibody-producing hybridomas such that the antibodies  
CC are presented at the surface of the hybridomas by an antibody-binding  
CC protein (I); and (ii) binding the antibody to antigens (Ag). The  
CC invention also describes antibody-binding proteins (I) that comprise a  
CC combination of the signal peptide of a murine immunoglobulin (Ig) kappa  
CC chain or a murine MHC (major histocompatibility complex) Class I k(k)  
CC molecule; an antibody-binding site of proteins A, G, L or Ig, and the  
CC transmembrane domain of PDGFR (platelet-derived growth factor receptor)  
CC or CD52. The method is used to select Mab with specificity for particular  
CC antigens. Mab can be selected without separate culture of hybridomas, and  
CC selection can be made against many antigens in a library, optionally on  
CC the basis of strength of affinity for a particular antigen. Complex  
CC mixtures of hybridomas can be used for selection, reducing the time and  
CC cost involved in Mab selection. This sequence represents the bla protein  
CC protein contained in the expression vector pSEX11G2 which contains the  
CC bla protein, Neo-R and protein G described in the method of the invention  
XX  
SQ Sequence 286 AA;  
Query Match 98.9%; Score 1330; DB 3; Length 286;  
Best Local Similarity 98.9%; Pred. No. 2.2e-129;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGEILLESFRSEERPEPMSTFKVLLCGAVLSRID 60  
Db HPE TLVKVDAEDQLGARVGYIELDINSGEILLESFRSEERPEPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KELTSALFNMGDHTVRLDRWEPELNEALPNDERDTTPVAMATTLRKLLTGELLTLASRQ 180  
Db KELTSALFNMGDHTVRLDRWEPELNEALPNDERDTTPVAMATTLRKLLTGELLTLASRQ 203  
QY 181 QLIDWMEADKYAGPLLRSALPAGWFIADKSGAGERGSRGIITAAIGPDGKPSRIIVITYTTG 240  
Db QLIDWMEADKYAGPLLRSALPAGWFIADKSGAGERGSRGIITAAIGPDGKPSRIIVITYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db SQATMDERNRQIAEIGASLIKHW 266

Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 14

AAB50898

ID AAB50898 standard; protein; 286 AA.

XX

AC AAB50898;

XX

DT 20-MAR-2001 (first entry)

XX

DE Protein encoded by bla resistance marker of integration vector pLO12306.

XX

KM bla resistance marker; recombinant host cell; saccharification;

KW fermentation; polysaccharase; oligosaccharide degradation; celZ gene;

KM glucanase; integration vector; pLO12306.

XX

OS Unidentified.

XX

PN WO200071729-A2.

XX

PD 30-NOV-2000.

XX

PF 26-MAY-2000; 2000WO-US014773.

XX

PR 26-MAY-1999; 99US-0136376P.

XX

PA (UYFL ) UNIV FLORIDA RES FOUND.

XX

PI Ingram LO, Zhou S;

XX

DR WPI; 2001-032043/04.

DR N-PSDB; AAC91455.

XX

PT Recombinant host cells useful for producing polysaccharase for degrading

PT oligosaccharides, comprises a first heterologous polynucleotide encoding

PT polysaccharase under control of surrogate promoter.

XX

PS Disclosure; Page 82-83; 87pp; English.

XX

CC The present sequence is given in a specification relating to a

CC recombinant host cell suitable for simultaneous saccharification and

CC fermentation. The host cell contains at least one heterologous

CC polynucleotide encoding a polysaccharase under the transcriptional

CC control of a surrogate promoter capable of increasing expression of the

CC polysaccharase. The host cell also contains a second heterologous

CC polynucleotide encoding a secretory polypeptide to facilitate the

CC secretion of the expressed polysaccharase. The recombinant host cell is

CC useful for producing polysaccharase which is useful for enzymatically

CC degrading oligosaccharides such as lignocellulose, hemicellulose,

CC cellulose, pectin or their combinations, and fermenting the product to

CC ethanol, by simultaneous saccharification and fermentation processes. The

CC present sequence is encoded by an integration vector which was introduced

CC into cells to generate recombinant host cells. The vector contains a

CC surrogate promoter from *Zymomonas mobilis*, the *celZ* gene from *Erwinia*

CC *chrysanthemi*, resistance markers *bla* and *tet*, and *Klebsiella oxytoca*

CC target sequence

XX

SQ Sequence 286 AA;

QY Query Match 98.9%; Score 1330; DB 4; Length 286;

Db Best Local Similarity 98.9%; Pred. No. 2.2e-129;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGILESFRSEERFPMMSTFKVLLCGAVLSRID 60

Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGILESFRSEERFPMMSTFKVLLCGAVLSRID 83

QY 61 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 120

Db 84 AGQEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTTGGP 143

QY 121 KELTSALFHNMGDHYTRLDRWEPELNEAIPNDERDITTPVAMATTLTKLLTGELLTLASRQ 180

Db 144 KELTSALFHNMGDHYTRLDRWEPELNEAIPNDERDITTPVAMATTLTKLLTGELLTLASRQ 203

QY 181 QLIDWMEADKVA GPELLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIWVYTTG 240

Db 204 QLIDWMEADKVA GPELLRSALPAGWFIADKSGAGERSRGIIAALGPDGKPSRIWVYTTG 263

QY 241 SQATMDERNRQIAEIGASLIKHW 263

Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 15

AAB31173

ID AAB31173 standard; protein; 286 AA.

XX

AC AAB31173;

XX

DT 02-APR-2001 (first entry)

XX

DE Amino acid sequence of a beta lactamate protein.

XX

KW Growth rate; death rate; reporter gene; luminescent protein;

KW fluorescent product; luciferase; green fluorescent protein; GFP.

XX

OS Unidentified.

XX

PN WO200075367-A1.

XX

PD 14-DEC-2000.

XX

PF 07-JUN-2000; 2000WO-FI000507.

XX

PR 07-JUN-1999; 99FI-00001296.

XX

PA (LILI/) LILIUS E.

PA (VIRT/) VIRTA M.

XX

PI lilius E, Virta M;

XX

DR WPI; 2001-061737/07.

DR N-PSDB; AAC86954.

XX

PT Assessing growth and death rates of a micro-organism in a desired

PT environment, by introducing 2 reporter genes encoding luminescent and

PT fluorescent products and detecting luminescent fluorescence.

XX

PS Disclosure; Page 28-29; 32pp; English.

XX

CC The specification describes a method for assessing the growth rate and

CC death rate of a micro-organism within a predetermined time period in a

CC desired environment. The method comprises introducing at least two

CC reporter genes encoding luminescent and/or fluorescent products into the

CC micro-organisms, incubating the micro-organism within the desired

CC environment, and detecting luminescence and/or fluorescence after a

CC predetermined time period. Use of two different markers within a micro-

CC organism enables the differentiation between growth and death rates. The

CC method is used to assess the growth rate and death rate of a micro-

CC organism within a predetermined time period in a desired environment. The

CC present sequence represents a beta-lactamate protein, and is encoded by a

CC plasmid which encodes luminescent and fluorescent proteins, and is used

CC in the method of the invention

XX

SQ Sequence 286 AA;

QY Query Match 98.9%; Score 1330; DB 4; Length 286;

Db Best Local Similarity 98.9%; Pred. No. 2.2e-129;

Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGILESFRSEERFPMMSTFKVLLCGAVLSRID 60

Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGILESFRSEERFPMMSTFKVLLCGAVLSRID 83

QY	61	AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP	120
Db	84	AGQEQIGRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAATMSDNTAANLLTTIGSP	143
QY	121	KEITAFIHNMGDHYTRLDWEPELINEAIPNDERDTPVAMATTLRKLLTGELLTIASRQ	180
Db	144	KEITAFIHNMGDHYTRLDWEPELINEAIPNDERDTPVAMATTLRKLLTGELLTIASRQ	203
QY	181	QIDWMEADKVAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVITYTTG	240
Db	204	QIDWMEADKVAGPILRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVITYTTG	263
QY	241	SOATMDERNRQIAEIGASLIKHW	263
Db	264	SOATMDERNRQIAEIGASLIKHW	286

Search completed: June 18, 2004, 19:08:00  
Job time : 63 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2004, 19:08:33 ; Search time 20 Seconds

(without alignments)  
594.865 Million cell updates/sec

Title: EPPER526106.PEP  
Perfect score: 1345  
Sequence: 1 hpetlvkxkdaedqlgarvg.....tmdernqiaigaslikhw 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 294345 seqs, 45236911 residues

Total number of hits satisfying chosen parameters: 294345

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending Patents\_AA New:\*  
1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep:\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep:\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep:\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep:\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep:\*  
6: /cgn2\_6/ptodata/2/paa/US10\_NEW\_COMB.pep:\*  
7: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	1330	98.9	286	5	US-09-490-324-265 Sequence 265, App
2	1330	98.9	286	5	US-09-490-324-362 Sequence 362, App
3	1330	98.9	286	6	US-10-416-708A-73 Sequence 73, Appl
4	1330	98.9	286	6	US-10-045-674A-523 Sequence 523, App
5	1330	98.9	299	5	US-09-490-324-285 Sequence 285, App
6	1330	98.9	299	5	US-09-490-324-298 Sequence 298, App
7	1330	98.9	299	5	US-09-490-324-300 Sequence 300, App
8	1329	98.8	286	6	US-10-842-534-9 Sequence 9, Appl1
9	1329	98.8	1293	6	US-10-668-035-57 Sequence 57, Appl1
10	1318	98.0	265	6	US-10-622-088-114 Sequence 114, App
11	1302	96.8	498	6	US-10-491-653-146 Sequence 146, App
12	343.5	25.5	306	6	US-10-724-972A-6154 Sequence 6154, Ap
13	175	13.0	290	6	US-10-414-532-65 Sequence 65, Appl
14	137	10.2	334	6	US-10-453-372-332 Sequence 332, App
15	137	10.2	841	6	US-10-453-372-334 Sequence 334, App
16	109	8.1	21	6	US-10-414-532-3 Sequence 3, Appl1
17	107.5	8.0	524	6	US-10-414-532-28 Sequence 28, Appl
18	102	7.6	432	1	PCT-US04-12717-118 Sequence 118, App
19	102	7.6	432	6	US-10-831-070-118 Sequence 118, App
20	102	7.6	432	7	US-60-546-745-58 Sequence 58, Appl
21	98	7.3	550	7	US-60-556-841-6264 Sequence 6264, Ap
22	98	7.3	552	7	US-60-556-841-3455 Sequence 3455, Ap
23	95.5	7.1	561	6	US-10-796-280-761 Sequence 761, App
24	94.5	7.0	410	6	US-10-474-792-90 Sequence 90, Appl
25	90	6.7	507	7	US-60-556-841-406 Sequence 406, App
26	90	6.7	1217	1	PCT-US04-02188-101 Sequence 101, App

27	90	6.7	1217	6	US-10-764-425-101	Sequence 101, App
28	89.5	6.7	363	7	US-60-556-841-4337	Sequence 4337, Ap
29	88.5	6.6	494	6	US-10-494-495-13	Sequence 13, Appl
30	87	6.5	451	6	US-10-474-792-390	Sequence 390, App
31	86.5	6.4	438	5	US-09-248-796A-19853	Sequence 19853, A
32	85.5	6.4	358	7	US-60-556-841-11741	Sequence 11741, A
33	85.5	6.4	551	6	US-10-767-701-45690	Sequence 45690, A
34	85	6.3	411	6	US-10-091-007A-190	Sequence 190, App
35	84.5	6.3	292	7	US-60-556-841-2583	Sequence 2583, Ap
36	84.5	6.3	363	7	US-60-556-841-2715	Sequence 2715, Ap
37	84.5	6.3	363	7	US-60-556-841-3776	Sequence 3776, Ap
38	83.5	6.2	331	6	US-10-494-672-294	Sequence 294, App
39	83.5	6.2	439	5	US-09-248-796A-19522	Sequence 19522, A
40	83	6.2	218	6	US-10-767-701-39284	Sequence 39284, A
41	82.5	6.1	657	7	US-60-556-841-6693	Sequence 6693, Ap
42	82	6.1	320	6	US-10-472-317-37	Sequence 37, Appl
43	82	6.1	421	7	US-60-556-841-12214	Sequence 12214, A
44	82	6.1	606	7	US-60-556-841-3226	Sequence 3226, Ap
45	81.5	6.1	314	1	PCT-US03-02038-220	Sequence 220, App

ALIGNMENTS

RESULT 1  
US-09-490-324-265  
; Sequence 265, Application US/09490324  
; GENERAL INFORMATION:  
; APPLICANT: Knappik, Achim  
; Pack, Peter  
; Ilag, Vic  
; Ge, Liming  
; Moroney, Simon  
; Plueckthun, Andreas  
; TITLE OF INVENTION: Protein/(Poly)peptide libraries  
; NUMBER OF SEQUENCES: 373  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
; STREET: 1251 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/490,324  
; FILING DATE: 24-Jan-2000  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,769  
; FILING DATE: 18-FEB-1998  
; APPLICATION NUMBER: EP 95 11 3021.0  
; FILING DATE: 18-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James F. Haley, Jr., Esq.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: MORPHO/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)596-9000  
; TELEFAX: (212)596-9090  
; INFORMATION FOR SEQ ID NO: 265:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 286 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 265:  
US-09-490-324-265  
Query Match 98.9%; Score 1330; DB 5; Length 286;



Best Local Similarity 98.9%; Pred. No. 1.7e-119; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 60  
 Db 24 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 83  
 QY 61 AGQEQGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
 Db 84 AGQEQGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
 QY 121 KELTAPFLHNMGDHVTIRLDKRWPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180  
 Db 144 KELTAPFLHNMGDHVTIRLDKRWPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 203  
 QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGRGSRGIIAALGPDGKPSRIVITYTTG 240  
 Db 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGRGSRGIIAALGPDGKPSRIVITYTTG 263  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 2  
 US-09-490-324-362  
 ; Sequence 362, Application US/09490324

GENERAL INFORMATION:  
 APPLICANT: Knappik, Achim  
 pack, Peter  
 Ilag, Vic  
 Ge, Liming  
 Moroney, Simon  
 Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries  
 NUMBER OF SEQUENCES: 373  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/490,324  
 FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/09/025,769  
 FILING DATE: 18-FEB-1998  
 APPLICATION NUMBER: EP 95 11 3021.0  
 FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: James F. Haley, Jr., Esq.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212)596-9000  
 TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 362:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 286 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: protein  
 SEQUENCE DESCRIPTION: SEQ ID NO: 362:

US-09-490-324-362

Query Match 98.9%; Score 1330; DB 5; Length 286;

Best Local Similarity 98.9%; Pred. No. 1.7e-119; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 60  
 Db 24 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 83  
 QY 61 AGQEQGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
 Db 84 AGQEQGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
 QY 121 KELTAPFLHNMGDHVTIRLDKRWPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180  
 Db 144 KELTAPFLHNMGDHVTIRLDKRWPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 203  
 QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGRGSRGIIAALGPDGKPSRIVITYTTG 240  
 Db 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGRGSRGIIAALGPDGKPSRIVITYTTG 263  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 3  
 US-10-416-708A-73  
 ; Sequence 73, Application US/10416708A

GENERAL INFORMATION:  
 APPLICANT: Wise, John G.

APPLICANT: Fromknecht, Katja  
 TITLE OF INVENTION: CREATION AND IDENTIFICATION OF PROTEINS HAVING NEW DNA BINDING  
 TITLE OF INVENTION: SPECIFICITIES  
 FILE REFERENCE: 37779-0004

CURRENT APPLICATION NUMBER: US/10/416,708A  
 CURRENT FILING DATE: 2004-01-28  
 NUMBER OF SEQ ID NOS: 89  
 SOFTWARE: Patentin version 3.2

SEQ ID NO 73  
 LENGTH: 286  
 TYPE: PRT  
 ORGANISM: Artificial Sequence

FEATURE:  
 OTHER INFORMATION: Synthetic Construct

US-10-416-708A-73

Query Match 98.9%; Score 1330; DB 6; Length 286;

Best Local Similarity 98.9%; Pred. No. 1.7e-119; Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 60  
 Db 24 HPETLVKVKDAEDQLGARVGYIELDINSGEILESFRSEERFPMMSTFKVLLCGAVLSRID 83  
 QY 61 AGQEQGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
 Db 84 AGQEQGLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
 QY 121 KELTAPFLHNMGDHVTIRLDKRWPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180  
 Db 144 KELTAPFLHNMGDHVTIRLDKRWPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 203  
 QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGRGSRGIIAALGPDGKPSRIVITYTTG 240  
 Db 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGRGSRGIIAALGPDGKPSRIVITYTTG 263  
 QY 241 SQATMDERNRQIAEIGASLIKHW 263  
 Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 4  
 US-10-045-674A-523  
 ; Sequence 523, Application US/10045674A

GENERAL INFORMATION:  
APPLICANT: LADNER, ROBERT C.  
APPLICANT: COHEN, EDWARD H.  
APPLICANT: NASTRI, HORACIO G.  
APPLICANT: ROOKEY, KRISTIN L.  
APPLICANT: HOET, RENE  
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.  
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING  
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY  
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL  
TITLE OF INVENTION: LIBRARIES  
FILE REFERENCE: DYAX/002 CIP2  
CURRENT APPLICATION NUMBER: US/10/045,674A  
CURRENT FILING DATE: 2001-10-25  
PRIOR APPLICATION NUMBER: 06/198,069  
PRIOR FILING DATE: 2000-04-17  
PRIOR APPLICATION NUMBER: 09/837,306  
PRIOR FILING DATE: 2001-04-17  
NUMBER OF SEQ ID NOS: 635  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 523  
LENGTH: 286  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Vector pCESS  
OTHER INFORMATION: protein sequence  
US-10-045-674A-523

Query Match 98.9%; Score 1330; DB 6; Length 286;  
Best Local Similarity 98.9%; Pred. No. 1.7e-119;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQIGRRIRHSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRRIRHSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KETLAFILNMGDHVTSLDREPELNEAIPNDERDTTPVAMATTLRKLLTGLLTLASRQ 180  
Db 144 KETLAFILNMGDHVTSLDREPELNEAIPNDERDTTPVAMATTLRKLLTGLLTLASRQ 203  
QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIILALGPDGKPSRIVIYTTG 240  
Db 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIILALGPDGKPSRIVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 5  
US-09-490-324-285  
Sequence 285, Application US/09490324  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/490,324  
FILING DATE: 24-Jan-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/025,769  
FILING DATE: 18-FEB-1998  
APPLICATION NUMBER: EP 95 11 3021.0  
FILING DATE: 18-AUG-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: James F. Haley, Jr., Esq.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: MORPHO/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 285:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 299 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 285:  
US-09-490-324-285

Query Match 98.9%; Score 1330; DB 5; Length 299;  
Best Local Similarity 98.9%; Pred. No. 1.9e-119;  
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 60  
Db 24 HPETLVKVKDAEDQLGARVGYIELDLSNGEILLESFRSEERFPMSTFKVLLCGAVLSRID 83  
QY 61 AGQEQIGRRIRHSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120  
Db 84 AGQEQIGRRIRHSQNDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143  
QY 121 KETLAFILNMGDHVTSLDREPELNEAIPNDERDTTPVAMATTLRKLLTGLLTLASRQ 180  
Db 144 KETLAFILNMGDHVTSLDREPELNEAIPNDERDTTPVAMATTLRKLLTGLLTLASRQ 203  
QY 181 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIILALGPDGKPSRIVIYTTG 240  
Db 204 QLIDWMEADKVAGPLLRSLPAGWFIADKSGAGERSRGIILALGPDGKPSRIVIYTTG 263  
QY 241 SQATMDERNRQIAEIGASLIKHW 263  
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 6  
US-09-490-324-298  
Sequence 298, Application US/09490324  
GENERAL INFORMATION:  
APPLICANT: Knappik, Achim  
Pack, Peter  
ilag, Vic  
Ge, Liming  
Moroney, Simon  
Plueckthun, Andreas  
TITLE OF INVENTION: Protein/(Poly)peptide libraries  
NUMBER OF SEQUENCES: 373  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10021

```

;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
;
; INFORMATION FOR SEQ ID NO: 298:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 298:
US-09-490-324-298
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```

Query Match          98.9%; Score 1330; DB 5; Length 299;
Best Local Similarity 98.9%; Pred.No.1.9e-119;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY      1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMSTFKVLLCGAVLSRID 60
      24 HPETLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83
Db
QY      61 AGQEQIGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
      84 AGQEQIGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143
Db
QY      121 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180
      144 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 203
Db
QY      181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYG 240
      204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYG 263
Db
QY      241 SQATMDERNRQIAEIGASLIKHW 263
      264 SQATMDERNRQIAEIGASLIKHW 286
Db
```

RESULT 7  
US-09-490-324-300

```

; Sequence 300, Application US/09490324
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
```

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;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
;
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
;
; INFORMATION FOR SEQ ID NO: 300:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 300:
US-09-490-324-300
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Query Match          98.9%; Score 1330; DB 5; Length 299;
Best Local Similarity 98.9%; Pred.No.1.9e-119;
Matches 260; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY      1 HPETLVKVKDAEDQLGARVGYIELDLSNGEILSEFRSEERFPMSTFKVLLCGAVLSRID 60
      24 HPETLVKVKDAEDQLGARVGYIELDLSNGKILESFRPEERFPMSTFKVLLCGAVLSRID 83
Db
QY      61 AGQEQIGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
      84 AGQEQIGRIHYSONDLVEYSPYTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143
Db
QY      121 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180
      144 KELTSALHNMGDHVTSLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 203
Db
QY      181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYG 240
      204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYG 263
Db
QY      241 SQATMDERNRQIAEIGASLIKHW 263
      264 SQATMDERNRQIAEIGASLIKHW 286
Db
```

RESULT 8  
US-10-842-534-9

```

; Sequence 9, Application US/10842534
; GENERAL INFORMATION:
; APPLICANT: Stewart, Francis
; APPLICANT: Zhang, Youming
; APPLICANT: Buchholz, Frank
; TITLE OF INVENTION: NOVEL DNA CLONING METHOD
; FILE REFERENCE: 2923-618
; CURRENT APPLICATION NUMBER: US/10/842,534
; CURRENT FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/231,013
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 09/555,510
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: PCT/EP 98/07945
; PRIOR FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: EP 97121462.2
; PRIOR FILING DATE: 1997-12-05
```

; PRIOR APPLICATION NUMBER: EP 98118756.0
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)..(286)
; OTHER INFORMATION: bla gene on plasmid pBAD24-rectr at 3493-4353
US-10-842-534-9

Query Match 98.8%; Score 1329; DB 6; Length 286;
Best Local Similarity 98.5%; Pred. No. 2.2e-119;
Matches 259; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSERRFPMSTFKVLLCGAVLSRID 60
Db 24 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPERFPMSTFKVLLCGAVLSRVD 83
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
Db 84 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 143
QY 121 KETLAFHNMGDHYTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180
Db 144 KETLAFHNMGDHYTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 203
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVIYTTG 240
Db 204 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVIYTTG 263
QY 241 SQATMDERNRQIAEIGASLIKHW 263
Db 264 SQATMDERNRQIAEIGASLIKHW 286

RESULT 9
US-10-668-035-57
; Sequence 57, Application US/10668035
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; APPLICANT: Lowltz, Kevin P.
; TITLE OF INVENTION: Endogenous, Constitutively Activated G Protein-Coupled
; TITLE OF INVENTION: Orphan Receptors
; FILE REFERENCE: Aren0047
; CURRENT APPLICATION NUMBER: US/10/668,035
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: 60/094,879
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: 60/106,300
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/110,906
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 1293
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-668-035-57

Query Match 98.8%; Score 1329; DB 6; Length 1293;
Best Local Similarity 98.5%; Pred. No. 1.8e-118;
Matches 259; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSERRFPMSTFKVLLCGAVLSRID 60
Db 245 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPERFPMSTFKVLLCGAVLSRVD 304
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
Db 305 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 364
QY 121 KETLAFHNMGDHYTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180
Db 365 KETLAFHNMGDHYTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 424
QY 181 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVIYTTG 240
Db 425 QLIDWMEADKVAGPLLRSAIPAGWFIADKSGAGERSRGIIAALGPDGKPSRIVIYTTG 484
QY 241 SQATMDERNRQIAEIGASLIKHW 263
Db 485 SQATMDERNRQIAEIGASLIKHW 507

RESULT 10
US-10-622-088-114
; Sequence 114, Application US/10622088
; GENERAL INFORMATION:
; APPLICANT: Bennett, Robert P.
; APPLICANT: Welch, Peter J.
; APPLICANT: Harwood, Steven
; APPLICANT: Madden, Knut
; APPLICANT: Frimpong, Kenneth
; APPLICANT: Franke, Kenneth E.
; TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
; FILE REFERENCE: 0942.5450007
; CURRENT APPLICATION NUMBER: US/10/622,088
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: PCT/US03/22437
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/396,335
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/398,617
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: US 60/427,231
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/456,496
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US 60/474,940
; PRIOR FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 265
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of a polypeptide having beta-lactamase activi
US-10-622-088-114

Query Match 98.0%; Score 1318; DB 6; Length 265;
Best Local Similarity 98.1%; Pred. No. 2.2e-118;
Matches 258; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 HPETLVKVKDAEDQLGARVGYIELDLNSGEILESFRSERRFPMSTFKVLLCGAVLSRID 60
Db 3 HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPERFPMSTFKVLLCGAVLSRVD 62
QY 61 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 120
Db 63 AGQEQIGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGP 122
QY 121 KETLAFHNMGDHYTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 180
Db 123 KETLAFHNMGDHYTRLDRWEPELNEAIPNDERDITTPVAMATTLRKLLTGELLTLASRQ 182

QY	181	QLIDWMEADKVAGPELLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG	240
Db	183	QLIDWMEADKVAGPELLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTG	242
QY	241	SQATMDERNRQIAEIGASLIKH	263
Db	243	SQATMDERNRQIAEIGASLIKH	265

RESULT 11  
US-10-491-653-146

```

; Sequence 146, Application US/10491653
; GENERAL INFORMATION:
; APPLICANT: Breiting, Frank
; APPLICANT: Moldenhauer, Gerhard
; APPLICANT: Poustka, Annemarie
; APPLICANT: Kuhlwein, Thorsten
; APPLICANT: Luttgau, Sandra
; TITLE OF INVENTION: Method for Producing Protein Libraries and for Selecting Proteins
; TITLE OF INVENTION: From Said Libraries
; FILE REFERENCE: 4121-162
; CURRENT APPLICATION NUMBER: US/10/491,653
; CURRENT FILING DATE: 2004-04-01
; PRIOR APPLICATION NUMBER: EP 01123596.7
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP02/10852
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 151
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 146
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-491-653-146

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Query Match	96.8%;	Score 1302;	DB 6;	Length 498;
Best Local Similarity	98.5%;	Pred. No. 1.8e-116;		
Matches 257; Conservative	1;	Mismatches 3;	Indels 0;	Gaps 0;

QY	3	ETLVKVKDAEDQLGARVGYIELDLNGEILLESFRRSEERFPMNSTEKVLLCGAVLSRIDAG	62
Db	238	ETLVKVKDAEDQLGARVGYIELDLNGKILLESFRRPEERFPNMSTFKVLLCGAVLSRIDAG	297
QY	63	QEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSPE	122
Db	298	QEQLGRRIRHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGSPE	357
QY	123	LTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQL	182
Db	358	LTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTTPVAMATTLRKLLTGELLTLASRQL	417
QY	183	IDMWEADKVAQPLIRSAALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYTGSQ	242
Db	418	IDTMEADKVAQPLIRSAALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIIVITYTGSQ	477
QY	243	ATMDERNRQIAETIGASLIKHW	263
Db	478	ATMDERNRQIAETIGASLIKHW	498

RESULT 12  
US-10-724-972A-6154

```

; Sequence 6154, Application US/10724972A
; GENERAL INFORMATION:
; APPLICANT: Doucette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH03-16
; CURRENT APPLICATION NUMBER: US/10/724,972A

```

```

; CURRENT FILING DATE: 2003-12-01
; PRIOR APPLICATION NUMBER: 09/450,969
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 7544
; SEQ ID NO 6154
; LENGTH: 306
; TYPE: prt
; ORGANISM: S.epidermidis
US-10-724-972A-6154

```

Query Match	25.5%;	Score 343.5;	DB 6;	Length 306;
Best Local Similarity	31.6%;	Pred. No. 5.3e-25;		
Matches 81; Conservative	62;	Mismatches 108;	Indels 5;	Gaps 4;

QY		7	KVKDAEDÖL GARVGYIELDNLSGEILLESFRSEERFPMAMSTFKVLLCGAVLSRIDAGÖEÖL	66
Dö		51	ELNNLEKKYNANIGVAYALDTKSKEVK -FNADKRFAYSTSKAINSAILLEÖVP--YNNKL	107
QY		67	GRRIRHSÖNDLVEYSPTYEKHLTDGMTVRELCSAAITMSDNTAANLLTTIGGPKELTAIF	126
Dö		108	NKKVHINKDDIVAYSPLEKCVGKDITLKELEASMKSYSDNTANNKIINEIGIKIKIRR	167
QY		127	LHNMGDHVTRLDRWEPELNEAI PNDERDTTTPVAMATTLRKULLTGELLTLASRÖQLIDMM	186
Dö		168	LKKLGDKVTNPVRXEIENLYSPEKSKDOSTPAAFGKITLNKL IANGKLSKNKNFLDLM	227
QY		187	EADKVAGPLLRSALPAGWFIADKSG-AGERGSRGIIAALGPDGKPSRIWITYTTSQATM	245
Dö		228	LNNKNGDTLIKDGVPKDYKVAADKSGQAITYASRNDAFVFPRKÖSEPILLVFTTNKONKS	287
QY		246	DERN-RÖIAIEIGASLI 260	
Dö		288	DKPNDKLISE TAKNVI 303	

## RESULT 13

```

US-10-414-532-65
; Sequence 65, Application US/10414532
; GENERAL INFORMATION:
; APPLICANT: CURTISS III, ROY
; APPLICANT: KANG, HO YOUNG
; TITLE OF INVENTION: IMPROVED IMMUNOGENIC COMPOSITIONS AND VACCINES COMPRISING
; TITLE OF INVENTION: CARRIER BACTERIA THAT SECRETE ANTIGENS
; FILE REFERENCE: 56029-40437
; CURRENT APPLICATION NUMBER: US/10/414,532
; CURRENT FILING DATE: 2003-04-15
; PRIOR APPLICATION NUMBER: 60/372,710
; PRIOR FILING DATE: 2002-04-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 65
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Protein
; OTHER INFORMATION: sequence of blaSS-pspA-EF5668-bla C-term region in
US-10-414-532-65

```

Query Match	13.0%;	Score 175;	DB 6;	Length 290;
Best Local Similarity	24.1%;	Pred. No. 6.7e-09;		
Matches 76;	Conservative 38;	Mismatches 101;	Indels 100;	Gaps 10;

```
QY      1 HPEITLVKVKDAEDQLGA--RVGYIELDNLNGEILSEFRSEERFPMSTFKVLLCGAVISR 58
        |||||         |   |   |   |   |   |   |   |   |   |   |   |   |
Db      24 HPEITLVKVKDAEEFLQASNESQKEADKKIKEATQ--RKDEAEAAAFATIRTTIVPEPSE 81
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```

QY      59 I-----DAGQEQLRRIHYSQNDLVEYSPTYEKHLTDGMTRELCSAA 101
      :      :      :      :      :      :      :      :      :
Db      82 LAETKKKAAEATKEAEVAKKKSEEAKEVEVEKNKILLEQDAENK-----K 127

QY      102 ITMSDNTAANLLTTTGGPKELTAFLHMGDHTRLDRWEPEINEAI PNDERDTTPVAM 161
      | : | : |      :      :      :      :      :      :      :
Db      128 IDVLQNKVADL-----EKGIAPYQNEVAELNKEIARLQSDLKDAENNVED-----YI 175

QY      162 ATTRLKLLTGELLTLASRQQLIDMWEADKVAGPLLRSA LPA GWFIADKSGAGERGSGRIT 221
      | : : : :      :      :      :      :      :      :      :
Db      176 KEGLEQAI TNKKALATLTTQONIDKTQKD-----LEDA-----ELELEKVL 215

QY      222 AALGPDGK-----PSRIVITYTGS-----QATMDER 248
      | : | : |      :      :      :      :      :      :
Db      216 ATLDPBGKTDQDELDEKAAEAEELNEKEVALQNOVAELLEELS KUDNLKDAETTLQATMDER 275

QY      249 NRQIAEIGASLTKHW 263
      |||||
Db      276 NRQIAEIGASLTKHW 290

```

```

RESULT 14
US-10-453-372-332
; Sequence 332, Application US/10453372
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 332
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-332

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Query Match	10.2%;	Score 137;	DB 6;	Length 334;
Best Local Similarity	47.9%;	Pred. No. 3.5e-05;		
Matches 35; Conservative	6;	Mismatches 10;	Indels 22;	Gaps 2;

```
QY      3 ETIVKVKDAEDÖLGARVGYTELDINSGEILLESFRSEERPPMSTFKVLLCGAVLSRIDAG 62
        ||||| : |
Db     38 ETIVKVKDAEDÖLGARVGYTELDINSGK-ETFLVN-----EAT 75
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QY 63 QEOLGRRIHYSQN 75  
| : : : |  
Db 76 GETSGDNVHSHRN 88

```

RESULT 15
US-10-453-372-334
; Sequence 334, Application US/10453372
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 334
; LENGTH: 841
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-334

```

Query Match	10.2%;	Score 137;	DB 6;	Length 841;
Best Local Similarity	47.9%;	Pred. No. 0.00013;		
Matches 35; Conservative	6;	Mismatches 10;	Indels 22;	Gaps 2;

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QY      3 ETIVKVKDAEDQLGARVGYIELDLNSGELLESRSEERFPMSTMFKLLCGAVLSRIDAG 62  
        ||||| |
        |||||  
        ||||| : |  
        |||||  
Db    38 ETIVKVKDAEDQLGARVGYIELDLNNGK--ETFLPNE-----EAT 75
```

```

QY      63 QEQLGRRIHYSQN 75
      76 | : : : |
Db      76 GETSGDNVTHSRN 88

```

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Search completed: June 18, 2004, 19:14:26
Job time : 22 secs
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